24, Appi 6, Appli

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CLASSIFICATION:
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 Command line parameters:

WODEL-frame+_n2p.model -DEV-x1h
-0-Ycgn2_1/05PO_Spool_/US09661170/runat_04042003_090918_20329/app_query.fasta_1.2375
-0-Ycgn2_1/05PO_Spool_/US096661170/runat_04042003_090918_20329/app_query.fasta_1.2375
-1DB-Issued_Patents_AA -OFMT-fastan -SUFFIX=n2p.rai -MINMACH=0.1 -LOOPCL=0
-1DSTA-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MXX=100 -THR_NNS-humand.cdi
-NODE-LOCAL -OUTPR-pco -NORM=ext -THR_MXX=100 -THR_NN=0 -ALIGN=15
-USER-0509667170_eCGN 1_1_17_@runat_0404203_090918_20329 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                April 16, 2003, 16:09:35 ; Search time 22 Seconds (without alignments) 5988.902 Million cell updates/sec
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Sequence 3, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 4, Appli
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Sequence 4, Appli
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Sequence 3, Appli
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                                                                                                                                                                           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*

    protein search, using frame_plus_n2p model

                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-073-362-1
US-09-243-920-1
US-08-825-781-3
US-08-825-781-4
US-08-825-781-1
US-08-132-990A-8
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                                                                                                                                                                                                                                                                                            262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                      Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
                                                                                                                                                US-09-667-170A-440
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                    Run on:
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PCT-US92-09382-8 US-09-134-001C-4290 US-08-132-990A-4

PCT-US92-09382-4

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Sequence 3357, Ap
Sequence 3357, Ap
Sequence 3001, Ap
Sequence 2, Appl1
Sequence 462, App
Sequence 5030, Ap
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Sequence 2, Appli
Sequence 3771, Ap
Sequence 4175, Ap
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Sequence 4, Appli
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Sequence 10, Appl
Sequence 4, Appli
Sequence 11, Appl
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Sequence 6,
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US-09-134-001C-5370
US-09-134-001C-4475
US-09-134-001C-4428
US-08-132-900A-2
US-09-134-001C-3771
US-09-134-001C-4175
US-09-134-001C-4175
US-09-134-001C-4175
US-09-134-001C-4309
US-09-134-001C-3357
US-09-134-001C-3357
US-09-134-001C-5030
US-09-134-001C-5030
US-09-134-001C-5030
US-09-134-001C-5030
US-09-134-001C-5030
US-09-134-001C-3581
US-09-134-001C-3581
US-09-134-001C-3581
US-09-134-001C-3501
US-09-134-001C-3501
US-09-134-001C-3501
US-09-134-001C-3501
US-09-134-001C-3501
US-09-134-001C-3501
US-09-134-001C-3501
US-09-134-001C-3109
US-09-134-001C-5109
US-09-134-001C-5109
US-09-134-001C-5109
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US-09-134-001C-5109
US-09-134-001C-5109
US-09-134-001C-5109
US-09-134-001C-5109
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APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE ON TIVENTION: AMINO ACID PERMEASE HOMOLOG
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-240-783B-4
US-08-753-985-10
US-09-084-813-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REPERENCE/DOCKET NUMBER: PF-0514 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/09/073,362
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; Patent No. 5942399
; GENERAL INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CON OPERATING SYSTEM:
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1054 ATTGTCACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAG 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 TyralaLysValValAlaLeuIleAlaIleIleValMetGlyLeuValLysLeuCysGln 216
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                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                            6.69e-113
1156.50
69.16%
           INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acids
                                                                                                                                                                                                                                           46.68%
                                                                                                                                                                                                                                                          28.07%
                                                                         single
                                                                     STRANDEDNESS: sin
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                   LIBRARY: GenBank
CLONE: 1665759
                                                          amino acid
                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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TELEX:
                                                            TYPE:
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1648 CCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACCAGA---ACATTACAAATAATAG 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1534 CTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1594 ATCACTCTGACTGGAGTCCCTGCGTATTATCTC-----TTTATTATATGGGACAAGAAA 1647
                                                                                                                                                                                        1294 TCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATGTTTTGCACCCTTTG 1353
                                                                                                                                                                                                                                                       1354 ACAAIGATAAIGCICTICTCIGGAGACCICGACAGICTITIGAAITICCICAGITITGCC 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 ilealaLeuSerGlyValProPheTyrPheMetGlyValTyrLeuProGluSerArgArg 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1174 TCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTG 1233
                                                                                                                            1234 TITGCIGTCTCCAGGITATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
                                                                                                                                                                                                                                                                                                                                                                                                       437 valpheLeuVailleValProLeuPheThrAspThrIleAsnSerLeuileGlyIleGly 456
1114 GAGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTTCTGAGCGGCTACTGGGAAATTC 1173
                                                                                                                                                                                                                                                                         AMINO ACID PERMEASE HOMOLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ for Windows Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/243,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/073,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09243920 Patent No. 5981242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L. APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1705 GAAGTIGIACCAGAAGAAGAT 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 CysvalLeuThrGluLeuAsp 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Diskette
IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 POR CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94304
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334 GAGAAAGTGCAGCTGAAGAAGAGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 393
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|17 GluAlaPheGlyGlyPheIleAlaPheIleArgLeuTrpValSerLeuLeuValValGlu 136
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| 137 ProThrGlyGlnAlaIleIleAlaIleThrPheAlaAsnTyrIleIleGlnProSerPhe 156
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Mismatches:
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                                                                                                                                                                                                                                                                             Length:
               NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0514 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                             Gaps:
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1156.50
69.168
46.688
28.078
                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   single
                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                              linear
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Best Local Similarity:
Query Match:
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994 ACTGAAGAAGTAGAAAAACCTGAAAAAACCATTCCCCTTGCAATATGTATATCCATGGCC 1053
                                                         1054 ATTGTCACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAG 1113
                                                                                                                 1114 GAGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGGGGCTACTGGGAAATTC 1173
                                                                                                                                                                            1174 TCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGT 1233
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                1294 TCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTG 1353
                                                                         1354 ACAATGATAATGCTCTTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCC 1413
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| 457 IlealaLeuSerGlyValProPheTyrPheMetGlyValTyrLeuProGluSerArgArg 476
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477 ProLeuPhelleArgAsnValLeuAlaAlaIleThrArgGlyThrGlnGlnLeuCysPhe 496
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1705 GAAGTTGTACCAGAAGAAGAT 1725
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Patent No. 5942399
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COMPUTER: IBM COmpatible
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MEDIUM TYPE: Diskett
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790 GCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATAATTATAGTC 849
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OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0514 US
PELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/073,362
                                                                                                                                                                                                                                                                                                                                                                                                                                              2.85e-110
                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
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68.00%
45.05%
27.46%
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     ESOGTUT02
                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                     2667831
                                                                               CLASSIFICATION:
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                                                                                                                             FILING DATE:
                                                                    FILING DATE
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1510 CCAGCITIGITITICCTICACAIGCCTCTICAIGGITGCCCTTICCCTCTAITCGGACCCA 1569
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                                                                                                                                                                                                                                                                                                      321 PhedlyGlyLeuAsnAlaSerIleValAlaAlaSerArgLeuPhePheValGlySerArg 340
                                                                                                                                                                                                                                   221 SerSerPheAlaValGlyAspIleAlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSer 240
                            201 AladiyilevalArgLeuGlyGinGlyAlaSerThrHisPheGluAsnSerPheGluGly 220
                                                                     910 AGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTATGCATATGCT 969
850 CCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGA 909
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APPLICANT: Corley, Neil C.
TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
TITLE OF SEQUENCES: 3
CORRESPONDEMCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09243920 Patent No. 5981242
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310 GGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTG 369
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| 121 TrpThrSerLeuLeullelleGluProThrSerGlnAlaIleIleAlaIleThrPheAla 140
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214
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149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/243,920
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                                                                                                                                                                                                                                                     NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0514 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/073,362
: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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68.00%
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27.46%
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                                                                                                                                                                                  CLASSIFICATION:
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LIBRARY: ESUGAL
TAME: 2667831
                                           USA
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                                                       94304
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                                                                                                                                                                        FILING DATE
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970 GGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAAACCATTCCC 1029
730 ATTACAGCIGIGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGC 789
                                 161 LeualaalaalacysileCysLeuLeuThrPheileAsnCysAlaTyrValLysTrpGly 180
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                                                                           790 GCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGGAATTCTGATAATTATAGTC 849
                                                                                                                181 ThrLeuValGlnAspIlePheThrTyrAlaLysValLeuAlaLeuIleAlaValIleVal 200
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| 421 ProlleValPheCysLeuCysThrIlePheLeuValAlaValProLeuTyrSerAspThr 440
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; Patent No. 5843727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN TUMOR-ASSOCIATED MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-667-170A-440 (1-2239) x US-08-825-781-3 (1-241)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
Indels:
                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,781
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                                                                                     E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                              PF-0262 US
                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 amino acids
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68.49%
47.90%
15.07%
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                                                                                                                                                                                                                                                                                       Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: GenBank
CLONE: 392990
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Query Match:
                                                                                                                      Palo Alto
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
GENERAL INFORMATION:
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                                                                                                                                                       USA
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1609 GTCCCTGCGTATTATTATTATTATGGGACAAGAAACCCAGGTGGTTTAGAATAATG 1668
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                                                                               1369 ITCICIGGAGACCICGACAGICITITGAAITICCICAGITITIGCCAGGIGGCITITIAII 1428
1309 CGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTC 1368
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203 LeuproValTyrPhePheGlyValTrpTrpLysAsnLysProLysTrpIleLeuGlnVal 222
                                                                                                                                                                                                                                                                                163 IleLysValAsnLeuAlaLeuProValPhePheIleLeuAlaCysLeuPheLeuIleAla 182
                                                                                                                                                                                                                                                                                                                                                |||||| |||:: |||::::|||||| |||||| :::
123 PheSerArgAspIlePheSerIleIleAsnPhePheSerPhePheAsnTrpLeuCysVal 142
                                                                                                                                                                                      1669 TCAGAGAAATAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAA 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 IlePheSerValThrValLeuCysGlnLysLeuMetGlnValValProGlnGlu 240
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APPLICANT: Hillman.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN TUMOR-ASSOCIATED MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,781 FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOKNEY AND TOWN J. NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0262 US
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; Sequence 4, Application US/08825781
; Patent No. 5843727
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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LENGTH: 241 amino acids
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PRIOR APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskett
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CLONE: 181908
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1009 AACCCTGAAAAAACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGC 1068
                                                                                                                                                                                                                            1069 TATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGTCA 1128
                                                                                                                                                                                                                                                                                   1129 AATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCG 1188
                                                                                                                                                                                                                                                                                                                                          1189 ATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGG 1248
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                                                                                                                                                                                                                                                                                                                                                                                                                   103 GinLeuLeuThrProValProSerLeuValPheThrCysValMetThrLeuLeuTyrAla 122
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                                                                                                                                                                                                                                                                                                                43 GluAlaValAlaValAspPheGlyAsnTyrHisLeuGlyValMetSerTrpIleIlePro 62
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203 LeuProValTyrPhePheGlyValTrpTrpLysAsnLysProLysTrpLeuLeuGlnGly 222
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN TUMOR-ASSOCIATED MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                    US-09-667-170A-440 (1-2239) x US-08-825-781-4 (1-241)
                                                                            Conservative:
Mismatches:
                                                  Length:
Matches:
                                                                                                          Indels:
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
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Patent No. 5843727
                                             4.29e-56
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68.07%
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14.93%
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                                                                   Percent Similarity:
                         Alignment Scores:
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STREET: 317
US-08-825-781-4
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1048 ATGCCCATTGTCACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAAT 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/825,781
FILING DATE: Herewith
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Matches:
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                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.44e-46
                                                                                                                                                                                                                                                                                                                                                              245 amino acids
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67.25%
44.54%
12.73%
                                                        Diskette
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                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                      linear
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LIBRARY: PANC.
2236771
                                                                                                                                                        CLASSIFICATION:
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             USA
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                                                    MEDIUM TYPE:
                                                                                                                                                                                                    FILING DATE:
                        94304
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CA
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            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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NERGL INFORMATION:
APPLICANT: MERUELCA DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
MINIE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
                                                                                                                       1588 TTCGTCATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTTATT-----ATATGGGAC 1641
                                                                                                                                                                                             1642 AAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACCAGAACATTACAAATAATA 1701
                                                   1528 ACATGCCTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGC 1587
                                                                                                                                                161 CysThrIlePheLeuValAlaValProLeuTyrSerAspThrIleAsnSerLeuIleGly 180
3: Pennie & Edmonds
1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                       1702 ---CTGGAAGTTGTACCAGAAGAAGAT 1725
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                                                                                                                                                                                                                                                                                                          221 CysmetSerValAlaAlaGluMetAsp 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/084,729 FILING DATE: 29-JUN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/899,075
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
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FILING DATE: 13-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08132990A Patent No. 5834589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-DEC-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
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FILING DATE: 11-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-0CT-1993
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; MOLECULE TYPE: protein
US-08-132-990A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUNDMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS:
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1108 GCTGAGGAGCTGCTGTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGA 1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AsnAsnAspThrLysGluGlyLysProGlyValGlyGlyPheMetProPheGlyPheSer 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 AsnValLeuValLeuGlyPheIleMetValSerGly------PheValLySGlySer 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 AlaGluAsnProAspIlePheAlaVallleIle------IleLeuIleLeuThr 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 SerTyrValThrValGlyGluLeuTrpAlaPheIleThrGlyTrpAsnLeuIleLeuSer 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   625 ---ATAATACGCCCTGCAGCTACTGCT---GTGATATCCCTGGCATTTGGACGCTACATT 678
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                                                                                                                                                                        331 AGAGAGAAAGTGGAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATT 390
                                                                                                                                                                                                                                                                                                                         451 AGCGTGGGCATGTCTCTGACCATC---TGGACGGTGTGTGGGGGTCCTGTCACTATTTGGA 507
                                                                                                                                                                                                         23 ArgGluGluThrArgLeuSerArgCysLeuAsnThrPheAspLeuValAlaLeuGlyVal 42
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58
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                                                                                                                                        US-09-667-170A-440 (1-2239) x US-08-132-990A-8 (1-629)
                                              Conservative:
                                                                    Mismatches:
                              Matches:
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              Length:
                2.93e-21
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43.16%
24.29%
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                                                                          Best Local Similarity:
                                                        Percent Similarity:
Alignment Scores:
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1168 ------AATTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGC 1215
                                                                                                       1216 TCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGT 1275
                                                                                                                                                                                1276 CACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTT 1335
                                                                                                                                                                                                                                                      1336 ATTGTTTTGCACCCTTTGACAATGATAATGCTCCTTCTCTGGAGACCTCGACAGTCTTTTG 1395
                                                                                                                                                                                                                                                                                                                             1396 AATTTCCTCAGTTTGCCAGGTGGCTTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTAT 1455
312 MetProTyrPheCysLeuAspAsnAsnSerProLeuProAspAlaPheLysHisValGly 331
                                                                      332 TrpGluGlyAlaLysTyrAlaValAlaVaiGlySerLeuCysAlaLeuSer----Ala 349
                                                                                                                                         350 SerLeuLeuGlySerMetPheProMetProArgvalIleTyrAlaMetAlaGluAspGly 369
                                                                                                                                                                                                         ||| ::: |||::: ||| 370 LeuLeuPheLysPheLeuAlaAsnValAsnAspArgThrLysThrProllelleAlaThr 389
                                                                                                                                                                                                                                                                                        390 LeuAlaSerGlyAlaValAlaAlaValMetAlaPheLeuPheAspLeuLySASpLeuVal 409
                                                                                                                                                                                                                                                                                                                                                            410 AspLeuMetSerIleGlyThrLeuLeuAlaTyrSerLeuValAlaAlaCysValLeuVal 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application PC/TUS9209382
GENERAL INFORMATION:
APPLICANT: MENCELO, DANIEL
APPLICANT: YOSHHAOTO, TARAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
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APPLICATION NUMBER:
FILING DATE:
FILING DATE:

CLASSIFICATION:
ATTORNEY AATTORNEY
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
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INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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AMINO ACID
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Best Local Similarity:
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331 AGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATT 390
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                                                                                                                                                                                                                                  451 AGCGTGGGCATGTCTCTGACCATC---TGGACGGTGTGTGGGGGTCCTGTCACTATTTGGA 507
                                                                                                                                                                                                                                                                                                                        508 GCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATAT 567
                                                                                                                                                                                                                                                                                                                                                          81 GlyLeuCysTyrGlyGluPheGlyAlaArgValProLysThrGlySerAlaTyrLeuTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                  568 ATTITGGAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTC--- 624
                                                                                                                                                                                                                                                                                                                                                                                                                                             101 SerTyrValThrValGlyGluLeuTrpAlaPheIleThrGlyTrpAsnLeuIleLeuSer 120
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                                                                                     23 ArgGluGluThrArgLeuSerArgCysLeuAsnThrPheAspLeuValAlaLeuGlyVal 42
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43 GlySerThrLeuGlyAlaGlyValTyrValLeuAlaGlyAlaValAlaArgGlu----- 60
                                                                                                                                                                                                                                                             ::: ||| :::::: ||| 61 AsnAlaGlyProAlaILeValIleSerPheLeuIleAlaAlaAlaSerValLeuAla 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       760 GTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGC 819
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254 GlyValLeuSerGlyAlaAlaThrCysPheTyrAlaPheValGlyPheAspCysIleAla 273
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484 TGTGGGGTCCTGTCACTATTTGGAGCTTTGTTTTTGCTGAATTGGGAACAACTATAAAG 543

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1378 GAC-------CTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGG 1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                        805 TICITAACCTITIGCAAGCTCACAGCAAITCTGATAATTATAGTCCCTGGAGTTATGCAG 864
                                                                                                                                                                                                                                      166 PheSerAlaAsnLeuArgGlyLeuTicAlaProLeuGlyIle-----SerLeuProLys 183
                                                                                                                                                                                                                                                                                                                     184 SerLeuSerAsnProPheGlySerAsnGlyGlyValileAspIleIleAlaAlaVal 203
                                                                                                                                                                                                                                                                                                                                                             745 ATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATT 804
107 AlaAlaIleValAlaGlyLeuValAlaPheThrTyrAlaGluMetAlaSerThrMetPro 126
                                           544 AAAICIGGAGGICATIACACATATATTIGGAAGTCITIGGICCAITACCAGCTITIGIA 603
                                                                  604 CGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGCA 663
                                                                                                                                                            147 AlaGlyTrpAla---LeuLeuAlaGluTyrPheIleAlaValAlaPheValAlaSerGly 165
                                                                                                                                                                                                    664 TTTGGA------CGCTACATTCTGGAACCATTTTTATTCAATGTGAAATCCCTGAA 714
                                                                                                                                                                                                                                                                                 ----GCGATCAAGCTCATTACAGCTGTGGGC 744
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APPLICANT: LYND DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 TTACTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTT 423
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        1276 CACCTTCCAGAAATCCTCTCTCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTT 1335
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                                                                                                                   410 AspLeuMetSerIleGlyThrLeuLeuAlaTyrSerLeuValAlaAlaCysValLeuVal 429
                                              370 LeuLeuPheLysPheLeuAlaAsnValAsnAspArgThrLysThrProllelleAlaThr 389
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 4290, Application US/09134001C patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Staphylococcus epidermidis US-09-134-001C-4290
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43.39%
24.11%
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Best Local Similarity:
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Oy 1480 C Db 454 P	CATCGTCCTTTCAAGGTGCCCACTGTTCATCCCAGCTTTGTTTTCCTTCACA 1530 ::: :::	
1531 T		_
473 L	473 LeuValLeuLeuValPheTrpGlyLeuSerPheGlualaLysLeuTyrThrienTleuTleuA92	
1588 T		
493 P		
RESULT 11		_
duence	Sequence 4, Application US/08132990A	_
Patent No. GENERAL IN	atent No. 5834589 GENERAL INFORMATION.	
APPLICANT:	ANT: MERUELO, DANIEL	
APPLIC,	YOSHIMOTO, TAKAYUKI	
NUMBER	NUMBER OF SEQUENCES: 31	
CORRESI	PONDENCE ADDRESS:	
STRE	É	
CITY:	: New York	_
COUNTRY:	: ::	
ZIP:	10036	_
MEDIC	COMPUTER REALABLE FORM: MEDIUM TYPE: Floppy disk	
COMPL	UTER: IBM PC compatible	
SOFT	SOFTWARE: Patent In Release #1.24	
CURRENT	F APPLICATION DATA: ICATION NUMBER: 118 / 012 / 13 2 000.	_
FILIN	FILING DATE: 07-0CT-1993	
APPLI	APPLICATION DATA:	
FILIN PRIOR A	FILING DATE: 29-JUN-1993	
APPLI	APPLICATION NUMBER: PCI/US93/05569	
FILIN PRIOR A	FILING DATE: 11-JUN-1993 PRIOR APPLICATION DATA.	
APPLI	APPLICATION NUMBER: 07/899,075	_
FILIN PRIOR A	FILING DATE: 11-JUN-1992 IOR APPLICATION DATA.	_
APPLI	APPLICATION NUMBER: 07/806,178	
FILIN PRIOR A	FILING DATE: 13-DEC-1991 PRIOR APPLICATION DATA:	
APPLI(APPLICATION NUMBER: 07/627,950	_
FILING ATTORNE	FILING DATE: 14-DEC-1990 ATTORNEY/AGENT INFORMATION.	_
NAME:	Misrock, S. Leslie	_
REFERI	ARGITION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 8105-004-999	
FELECOMMUNICATE TELEPHONE	ATION INFORMATIO	_
TELEFAX:	AX: (212) 869-8864	
TELEX: FORMATIC	TELEX: 66441 PENNIE INFORMATION FOR SEC ID NO. 4.	-
SEQUENCE	SEQUENCE CHARACTERISTICS:	
TYPE: 6	H: 622 amino acids amino acid	_
STRANDEDN TOPOLOGY:	STRANDEDNESS: single TOPOLOGY: linear	
; MOLECULE TYPE: US-08-132-990a-4	E TYPE: protein	
3 1 1	P 47	
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1.41e - 20

Alignment Scores: Pred. No.:

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331 AGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATT 390
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                                                                                                              US-09-667-170A-440 (1-2239) x US-08-132-990A-4 (1-622)
                         Conservative:
Mismatches:
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                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                        1333 GTTATTGTTTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTT 1392
                                        1213 GGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAG 1272
                                                                                                                                                                                                                                                                         402 ValAspLeuMetSerIleGlyThrLeuLeuAlaTyrSerLeuValAlaAlaCysValLeu 421
                                                                                                                                                                                                         382 ThrValThrSerGlyAlaIleAlaAlaValMetAlaPheLeuPheGluLeuLysAspLeu 401
                                                                      343 ---SerLeuLeuGlySerMetPheProMetProArgVallleTyrAlaMetAlaGluAsp 361
                                                                                                                                         362 GlyLeuLeuPheLysPheLeuAlaLysIleAsnAsnArgThrLysThrProvalIleAla 381
       324 GlyTrpGluGluAlaLysTyrAlaValAlaIleGlySerLeuCysAlaLeuSerThr--- 342
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-667-170A-440 (1-2239) x PCT-US92-09382-4 (1-622)
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Conservative:
Mismatches:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Browdy and Neimark
419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application PC/TUS9209382
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: MEI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-5197
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Livnat, Shmuel REGISTRATION NUMBER: 33,949
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279.50
42.82%
24.00%
6.78%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT
                                                                                                                                                                                                                                                                                                                 1453 TATCTTCGATACAAA 1467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20004
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1213 GGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAG 1272
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331 AGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATT 390
                                                                                                           391 GGCACCATCATTGGAGCAGGAATCTTCATCTCCTAAGGGCGTGCTCCAGAACACGGGC 450
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                                                                                                                                                             43 GlySerThrLeuGlyAlaGlyValTyrValLeuAlaGlyAlaValAlaArgGlu----- 60
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                                                    23 ArgGluGluSerArgLeuSerArgCysLeuAsnThrTyrAspLeuValAlaLeuGlyVal 42
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Db 139 ThrValAlaGlyTrpAspValTyrIleThrGluIl	Oy 751 GTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTG	Qy 811 ACCTITIGCAAGCTCACAGCAATTCTGATAATTAT	AGAA	Oy 931 TTGCCACTGGCT	QY 964 TATGCTGGCTGGTTTACCTCACTTT	Oy 1009 Db 244	Qy 1066 GGCTATGTGCTGACAAATGTG	Oy 1108 GCTGAGGAGCTGCTTTCAAATGCAGTGCAGTG	1168	298	VI 1225 GGIGGIGGITGCTGCTCCAGGTTATTCTATGTTT	OY 1285 GAAATCCTCTCCATGATTCATGTCCGCAAGCACACTC	1345	1381 1381 378	QY 1441 GCTGGGCTGATTTATCTTCGATACAAATGCCCAGATA	QY 1498 CCACTGTTCATCCCAGCTTTGTTTTCCTTCATCATCATCTTGTTTTCCTTCATCATCATCATCATCATCATCATCATCATCA	Qy 1546GCCCTTTCCCTTATTCGGACCCATTA 	Oy 1597 ACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTAT	OY 1657 TTTAGAATAATGTCAGAGAAAATAACCAGAACATTA
362	<pre>Qy 1333 GTTATTGCACCCTTTGACAATGATAATGCTCTTCTGGAGACCTCGACAGTCTT 1392 ::: Db 382 ThrValThrSerGlyAlaIleAlaAlaValMetAlaPheLeuPheGluLeuLySAspLeu 40:</pre>		Oy 1453 TATCTTCGATACAA 1467 Db . 422 ValleuArgTyrGln 426	RESULT 13 US-09-134-001C-5370 ; Sequence 5370, Application US/09134001C ; Patent No. 6380770	GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO			10 ÷ =	; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5370	7.68e-15 Length:	Percent Similarity: 41.90% Conservative: 90 Best Local Similarity: 24.11% Mismatches: 193 Query Match: 5.45% Todals: 193	Gaps: S-09-134-001C-5270 /124	ي پ	OY 439 CAGAACACGCCACCACAGCATCTCACACATCTGACGACGACGTGTGGGGCTCTGTCA 498 11		OY 559 TACACATATATTTGGAAGTCTTTGGTCCATTACCACGTTTTGTACGAGGTCTGGGTGGAA 618 1:	E :	AGCTCATT ysLeuTyr	

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FILE REPRENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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PRIOR FILING DATE: 1997-11-08
PRIOR PLING DATE: 1997-18-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3778
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US-09-134-001C-3778
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Mismatches:
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PRILICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-08
                                                                                                        Sequence 4475, Application US/09134001C
Patent No. 6380370
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SEQ ID NO 4475
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Best Local Similarity:
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                1060 ACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTG 1119
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                                                                                                                                               188 AlaileLeuTyrIleValLeuGlnSerThrPheIleThrSerMetProSerSerMetLeu 207
                                                 168 GlulleLysAsnProGluLysAsnIleAlaArgGly1leVallleSerLeuThrLeuSer 187
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11gnment red. No.: core: Sizercent S	7.48e-12 Length: 477 196.00 Matches: 10 38.71% Conservative: 80 tty: 21.51% Mismatches: 21 tty: 4.76% Indels: 72	GGGAGTCTC ::: SHisIleSe	GGGCGTGCTCCAGAACACGGGCAGCGTGGCATGTCTCTGACCATCTGGACGGTGTGT 4 ::	GGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAA 5 ::: :::	CTGGAGGTCATTACACATATATTTGGAAGTCTTTGGTCCATTACCAGCTTTTGTACGA 6	TCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTG 660 	ATTTGGACGCTACATTCTGGAACCATTTTTATTCAATGTGAAAATCCCTGAACTTGCG 72	<pre>ICAAGCTCATTACAGCTGTGGGCATAACTGTAGTGGTGGTGCTGAATAGCATG 774 </pre>	CTGGAGCGCCGGATCCAGATTTCTTAACCTTTTGCAAGCTCACAGCAATT 83 ::: :: ::: ::	GGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAG 885 	CTTTAAAAGACGCCTTTTCAGGAAGAGAT	CGGTTGCCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTG	CTCAACTTGTTACTGAAGAGTAGAAACCCTGAAAAAACCATTCCCCTTGCAATA 10 ::: 	TATATCCATGGCCATTGTCACTGGCTATGTGCTGACAAATGTGGGCCTACTTTACG 10 ::: ::: sGlnValPheTrpArglieLeuLeuPheTyrIleLeuAlaIlePheIleIleGlyMet 28	TGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTT 1 	TTCTCATTAGCAGTTCCGATCTTT 11	TGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTTGCTGTCTCCAGGTTATTC 12 :: ::: :: :
Ilignment red, No. Sericota sericota sericota sericota sericota 330 330 330 342 447 447 447 447 447 547 547 547 547 547	Scores: imilarity: l Similari ch:		AAGGGCGTGC7 :: GlyGlyAlaI	GGGGTCCTGTC ::: GlyAlaMetVa	TCTGGAGGTCP SerGlySerPh	GTCTGGGTGGA GlyTrpAsnTy	GCATTTGGACG	TCAAG eProalaTr	AGTGTCAGCTG ServalArgva	TGATAATT :: leilePhe	AACTTTAAAGA GlyPheAs	AGTATTACGCG ::: SerLeuLeuSe	AC.		ACCATTAATGC: LeulleProTy:	TCTGAGCGGCT1 :: PheThrLeuVal	STFGCCCTCTCC
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322 IleLeuThrSerValLeuSerAlaGlyAsnSerGlyMetTyrAlaSerThrArgMetLeu 341
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Search completed: April 16, 2003, 16:27:03 Job time : 35 secs

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Command line parameters:
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-MODEL-framet-n2p. model -DEV-x1h
-MODEL-framet-n2p. model -DEV-x1h
-MODEL-framet-n2p. model -DEV-x1h
-UO-Cgn2_1/USPTO_spool/US09667170/runat_04042003_090919_20390/app_query.fasta_1.2375
-DB-Published_Applications_AA -QFMT-fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCLL-0 -LOOPEXT-0 -UNITS-bits -START-1.FBND-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MXX-100
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MXX-100
-WAXLEN-200000000 -USER-US09667170_eCGN_1_1_15_eTrunat_0404203_30919_22030
-NCPU-6 -ICQPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERX -NEG_SCORES-0 -WAIT -LONGLOG
-NCPU-6 -ICQPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERX -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP=10 -XGAPEXT-0.5 -FGAPOP=6
                                                                                                                                                                                                                                  (without alignments)
5169.450 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                              April 16, 2003, 16:10:40 ; Search time 65.5 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                           OM nucleic - protein search, using frame_plus_n2p model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Database: Published_Applications_AA:*

1: /cgn12_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/USOF_NEW_PUB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appl	Appı	Appl	Appı
	_	48,	φ. γ.	54,	3/,
	Description	Sequence 48,	Sednence	Sednence	Sednence
	ID	US-10-163-866-48	US-10-163-866-49	US-10-163-866-54	US-10-163-866-37
	DB	6	δ	σ	σ
	Query Match Length DB	501	501	507	524
æ		61.1	61.1	29.4	29.3
	Score		2519	1210.5	1206.5
	Result No.	1	7	3	4

38, Appl 41, Appl 41, Appl 42, Appl 43, Appl 45, Appl 45, Appl 47, Appl 47, Appl 47, Appl 47, Appl 47, Appl 47, Appl 58, Appl 58, Appl 58, Appl 58, Appl 58, Appl 59, Appl 51,	e 11388 e 12036 e 12844 6946, e 144, e 10265 e 5055,
0.163-866-38 0.163-866-40 0.163-866-42 0.163-866-42 0.163-866-42 0.163-866-43 0.163-866-44 0.163-866-44 0.163-866-45 0.163-866-45 0.163-866-45 0.163-866-45 0.163-866-45 0.163-866-45 0.163-866-45 0.9-925-297-747 0.9-925-297-747 0.9-815-242-1005 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1394 0.9-815-242-1393	US-09-815-242-11 US-09-815-242-12 US-09-815-242-12 US-09-738-626-694 US-09-801-368-14 US-09-815-242-10 US-09-815-242-10
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US-10-163-866-48

US-10-163-866-48

Sequence 48, Application US/10163866

Publication No. US20030027188A1

GENERAL INFORMATION:

APPLICANT: EXELIXIS, INC.

TILE OF INVENTION: SLC75 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

TILE OF INVENTION: SLC75 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

FILE REFERENCE: EX02-080C

CURRENT PELLING DATE: 2002-06-05

PRIOR PELLING DATE: 2001-06-05

PRIOR PELLING DATE: 2001-10-10

PRIOR PILLING DATE: 2001-10-10

PRIOR PILLING DATE: 2001-10-22

PRIOR PILLING DATE: 2001-10-22

PRIOR PILLING DATE: 2002-02-15

PRIOR PILLING DATE: 2002-02-15

PRIOR PILLING DATE: 2002-02-15

PRIOR FILLING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 54

SEQ ID NO 48

LENGTH: 501

TYPE: PRT

TYPE: PRT
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APPLICANT: EXELIXIS, INC.

TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EXO2-0805
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
PRIOR PELLING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR PRIOR PRILING DATE: 2001-10-22
PRIOR PRILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 54
SSOTT NO. 40
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Matches:
Conservative:
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; Publication No. US20030027188A1
; GENERAL INFORMATION:
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APPLICAMY: EXELIXIS, INC.

TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REPERENCE: EX02-080-C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR PLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-10-10
PRIOR PLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-25
PRIOR FILING DATE: 2001-10-25
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2002-02-15
1204 TCCTGCTTTGGCTCCATGAACGGTGTGTGTTTGCTGTCTCCAGGTTATTCTATGTTGCG 1263
                                                                            1264 TCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCT 1323
                                                                                                                                                    1384 GACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTTATTGGGCTGGCAGTTGCT 1443
                                                                                                                                                                                                                                                                                                          1444 GGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTG 1503
                        1504 TICATCCCAGCTITGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCATTCG 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1564 GACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATTAT 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1624 CTCTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACC 1683
                                                                                                                                                                                                                                                     1684 AGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAAGATAAGTTA 1731
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Matches:
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Publication No. US20030027188A1
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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1261 GCGTCTCCAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACAT 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        847 GTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAAGACGCCTTTTCA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 LeuLeuGlyPheValGlnIleGlyLysGlyAspValSerAsnLeuAspProAsnPheSer 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               547 TCTGGAGGTCATTACACATATTTTGGAAGTCTTTGGTCCATTACCAGCTTTTGTACGA 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAA 546
                                                                                                                                                                                                                                                                                                                                                                                                                   307 TCAGGAAGAGGACGTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTA 366
                                                                                                                                                                                                                 367 CTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCTCCT 426
                                                                                                                                                                                                                                                                                                     427 AAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTGTG 486
                                       247 CCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACGCCTTT 306
                                                                                                                                                                                                                                           73 ThrGlyValLeuLysGluAlaGlySerProGlyLeuAlaLeuValVrlTrpAlaAlaCys 92
                                                                               14 proAlaAlaGluGluLysGluGluAlaArgGluLysMetLeuAlaAlaLysSerAlaAsp 33
                                                                                                                                                       14 GlySerAlaProAlaGlyGluGly---GluGlyValThrLeuGlnArgAsnIleThrLeu 52
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US-09-667-170A-440 (1-2239) x US-10-163-866-54 (1-507)
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-086.

CURRENT APPLICATION NUMBER: US 60/296,076
PRIOR APPLICATION NUMBER: US 60/298,605
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-2
PRIOR FILING DATE: 2001-10-2
PRIOR FILING DATE: 2001-10-2
PRIOR PAPLICATION NUMBER: US 60/387,253
PRIOR APPLICATION NUMBER: US 60/357,560
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 64
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                                                                                             1381 CTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTATTGGGCTGGCAGTT 1440
1321 CCICTACCAGCIGITAIIGITIIGCACCCITIGACAAIGAIAAIGCICIICICIGGAGAC 1380
                                                                                                                                                                                                                       433 LeualaLeuProValPhePheIleLeualaCysLeuPheLeuIleAlaValSerPheTrp 452
                                                                                                                                                                                                                                                                                                                                                                                                                 453 LysThrProvalGluCysGlyIleGlyPheThrIleIleLeuSerGlyLeuProValTyr 472
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                                                                                                                              1681 ACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAA 1722
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51 GlySerAlaProAlaGlyGluGlyGluGlyValThrLeuGlnArgAsnIleThrLeu 69	367 CTGAGGGGACTCTCCATTATCATTGGCACCATGGAGCAGGAATCTTCATCTCTCT 426 11	TGACCATCTGGACGGTGTGT 48	STCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAA S	14	ATTT 6	CAATGTGAAATCCCTGAACTTGCGATCAAG 72	IGTCAGCTGG 78 rValLysAla 20	<pre>rCTGATAATTATA 84 : :: uAlaLeuIleIle 22</pre>	CCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCCTTTTCA 90 	<pre>rarggaargrar 96 :::::: SerGlyLeuPhe 26</pre>	10.	<pre>FGGCTATGTGCTGACA 10:</pre>	SCAGTGGCA 11. 	.141 GTGACCTTTTCTGAGCGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTGTTGCC 1200 	AGGTTATTCTATGTT 12 	CACACT 13: 	321 CCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGAC 1380 ::: :::	AGTT 14.
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TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EXO2-080.

FILE REFERENCE: EXO2-080.

CURRENT APPLICATION NUMBER: US/10/163,866

CURRENT FILING DATE: 2002-06-05

PRIOR PAPLICATION NUMBER: US 60/296,076

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-10-10

PRIOR PLICATION NUMBER: US 60/338,733

PRIOR PLICATION NUMBER: US 60/338,733

PRIOR FILING DATE: 2001-10-22

PRIOR PLICATION NUMBER: US 60/357,253

PRIOR FILING DATE: 2002-02-15

PRIOR FILING DATE: 2002-02-15

PRIOR FILING DATE: 2002-02-15
1441 GCTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCA 1500
                                                                          1501 CTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTAT 1560
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                  470 LysThrProValGluCysGlyIleGlyPheThrIleIleLeuSerGlyLeuProValTyr 489
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14 ProvalalaGluGluLysGluGluAlaArgGluLysMetLeuAlaSerLysArgAlaAsp 33
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                                                                                                                                                                                                                                                                                                               1681 ACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAA 1722
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; Publication No. US20030027188A1
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-10-163-866-38
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Pred. No.:
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US-10-163-866-38
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                                                  487 GGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAA 546
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APPLICANT EXELISIS, INC.

APPLICANT EXELISIS, INC.

TITLE OF INVENTION: SLC75 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EXO2-080C

CURRENT APPLICATION NUMBER: US/10/163,866

CURRENT FILING DATE: 2002-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-2

PRIOR FILING DATE: 2001-10-2

PRIOR FILING DATE: 2001-10-2

PRIOR FILING DATE: 2001-10-2

PRIOR FILING DATE: 2000-02-15

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                                        1201 CTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCCAGGTTATTCTATGTT 1260
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7S AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
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1681 ACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAA 1722
                           US-09-667-170A-440 (1-2239) x US-10-163-866-40 (1-515)
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PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2002-02-15
PRIOR PAPLICATION NUMBER: US 60/357,253
PRIOR PAPLICATION NUMBER: US 60/357,600
PRIOR PRIOR PILING DATE: 2002-02-15
PRIOR PRIOR PRIOR DATE: 2002-02-15
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                                                                                                                                          ; Sequence 40, Application US/10163866; Publication No. US20030027188A1; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7S AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
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                                 814 ITTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAA 873
                                                         874 GGTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG 933
                                                                                                                            177 LeuThrPheValAsnCysAlaTyrValLysTrpGlyThrArgValGlnAspThrPheThr 196
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                                                                             PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2002-02-15
FILE REFERENCE: EX02-080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
                                             CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/296,076
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-080C
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                                                                                                          .030 CTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAATGTGGCC 1089
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221 SerSerPheAlaValGlyAspIleAlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSer 240
                                                          1450 ATTTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATC 1509
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APPLICATION NUMBER: US 60/338,733
FILING DATE: 2001-10-22
APPLICATION NUMBER: US 60/357,253
FILING DATE: 2002-02-15
APPLICATION NUMBER: US 60/357,600
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; Publication No. US20030027188A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-080C
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PRIOR FILING DATE: 2001-10-12
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PRIOR FILING DATE: 2002-02-15
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Conservative:
                                                     Mismatches:
    65.52%
44.62%
26.74%
              Percent Similarity:
Best Local Similarity:
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-080C
                                        1273 GGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCT 1332
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328 GlyGlyValAsnGlySerLeuPheThrSerSerArgLeuPhePheAlaGlyAlaArgGlu 347
                                                                 368 LeuLeuPheThrCysIleSerThrLeuLeuMetLeuValThrSerAspMetTyrThrLeu 387
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PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR PLILING DATE: 2001-10-22
PRIOR APPLICATION UNMBER: US 60/357,253
PRIOR APPLICATION UNMBER: US 60/357,600
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION UNMBER: US 60/357,600
PRIOR FILING DATE: 2002-02-15
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Publication No. US20030027188A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 44
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                                    322 ITTTCAGGAAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCC 381
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-080C
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                                             1393 ITGAAITICCICAGITITGCCAGGIGGCITTITAITGGGCIGGCAGITGCIGGCCIGAIT 1452
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368 LeuLeuPheThrCysIleSerThrLeuLeuMetLeuValThrSerAspMetTyrThrLeu 387
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CURRENT FILING DATE: 2002-06-05
PRIOR FULING DATE: 2002-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-12
PRIOR PPLICATION NUMBER: US 60/338,733
PRIOR APPLICATION NUMBER: US 60/357,533
PRIOR APPLICATION NUMBER: US 60/357,503
PRIOR APPLICATION NUMBER: US 60/357,503
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR PRILING DATE: 2002-02-15
PRIOR PRILING DATE: 2002-02-15
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1546 GCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATC---ACTCTG 1602
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                                                                                                                                                                                                                                                                              AATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTC 825
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| 186 AsnSerLeuSerValArgLeuGlySerTyrValGlnAsnIlePheThrAlaAlaLysLeu 185
                                                  526 ITGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGT 585
                                                                                  86 LeuGlyThrMetIleThrLysSerGlyGlyGluTyrProTyrLeuMetGluAlaTyrGly 105
66 LeullelleTrpAlaAlaCysGlyValLeuAlaThrLeuGlyAlaLeuCysPheAlaGlu 85
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REPERENCE: EXO2-080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
                                  1603 ACTGGAGTCCCTGCGTATTATCTCTTTATTATGGGACAAGAAACCCAGGTGGTTTAGA 1662
                                                                                                  1663 AFAATGTCAGAGAAATAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAA 1722
426 LeuAlaProllelleSerLysProThrTrpGluTyrLeuTyrCysValLeuPhelleLeu 445
                                                                  446 SerGlyLeuLeuPheTyrPheLeuPheValHisTyr----LysPheGlyTrpAlaGln 463
                                                                                                                             464 LysIleSerLysProlleThrMetHisLeuGlnMetGluValValValProProGlu 483
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Mismatches:
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PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATCHTIN VERSION 3.1
LENGTH. 45
                                                                                                                                                                                                                                                                             Sequence 45, Application US/10163866
Publication No. US20030027188A1
GENERAL INFORMATION:
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Best Local Similarity:
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US-10-163-866-45
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946 TATTATGGAATGTATGCATATGCTGGCTTGTTTACCTCAACTTTGTTACTGAAGAAGTA 1005
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                                           706 ATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTA 765
                                                                        146 ProproginileValValLysCysLeuAlaAlaAlaAlaileLeuPheIleSerThrVal 165
                                                                                                      766 AATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTC. 825
                                                                                                                               166 AsnSerLeuSerValArgLeuGlySerTyrValGlnAsnIlePheThrAlaAlaLysLeu 185
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186 ValIleValAlaIleIleIleSerGlyLeuValLeuLeuAlaGlnGlyAsnThrLys 205
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406 ProlleLysValProValValIleProValLeuMetThrLeuIleSerValPheLeuVal 425
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC78 AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
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                                                                                                                                243 GluthraspProGlyLysLeualaValalaPheTyrSerGlyIlePheSerTyrAlaGly 262
                                853 GGAGTTATGCAGCTAAȚTAAAGGTCAAACGCÀGAACTTTAAAGACGCCTTTTCAGGAAGA 912
                                                   203 LysMetGlnAsnValPheWetPheThrLysIleGlyAlaLeuValLeuValIleIleVal 222
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; Publication No. US20030027188A1
; GENERAL INFORMATION:
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US-09-315-923-16
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Sequence 16, Application US/09815923
Sequence 16, Application No. US20020197644A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GILL, Sarjeet S.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of Insect Cell Membrane Transporters as No. US20020197644A1e1
TITLE OF INVENTION: Target Sites for Insecticides
FILE REFERENCE: 023070-093800US
FILE REFERENCE: US/09/815,923
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 20
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PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR APPLICATION NUMBER: US 60/357,260
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATCHIN VERSION 3.1
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252 AsnTyrValThrGluGluMetValAspAlaArgLysAsnLeuProArgAlaIlePheIle 271
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-MODEL=frame+_n2p.model -DEV=x1h
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
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/SIDS2/gcgdata//geneseq/geneseqp-embl/AA1997_DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998_DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998_DAT:
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            A_Geneseq_101002:*
Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Adminity cyconies, very prointeraction, very controller. Strong hammal projects are guilation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder;

KW inhibin; Chemotaxis; chemokinesis: thrombolusis: activin;
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Mismatches:

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cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                                   Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                   Claim 20; Page 286; 1963pp; English.
                                                                                                                                   Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                     e.g. arthritis and cancer -.
                                                                                                03-FEB-2000; 2000US-0496914.
                                                                                  05-FEB-2001; 2001WO-US03800.
                                                                                                        27-APR-2000; 2000US-0560875
                                                                                                                                                  WPI; 2001-457740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 AA;
                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                        N-PSDB; ABA09201
                                                       WO200157188-A2.
                                         Homo sapiens.
                                                                     09-AUG-2001.
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Conservative: Length:

466.00 100.00%

Score: Percent Similarity:

Alignment Scores:

Pred. No.:

Sednence

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Query Match:
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Companied in oncogenesis, cancer cell proliferation or metastasis.

Companied in oncogenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or agene therapy. Such conditions include conditions, e.g., by protein or agene therapy. Such conditions include conditions; e.g., mypopetides and activities may be used to promote verial and fungal infections in disorders (e.g., myeloid or propertic disorders (e.g., myeloid or proliferative retinopathy athrosoclerosis, coronary heart of surface repair (or nucleic acids encoding them) may be used to promote with growth. Polypeptides such proliferations in addition to immune disorders (e.g., capaling or promote cell growth. For 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
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1294 TCCATGATTCATGICCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTG 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1234 ITTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1054 ATTGTCACCATTGGCTATGTGCTGACAAATGTGGCCCTACTTACGACCATTAATGCTGAG 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1114 GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTC 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         994 ACTGAAGAAGTAGAAAACCCTGAAAAAACCATTCCCCTTGCAATATGTATTCCATGGCC 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                933
                                                                                                                                                                                                                                                                                                          814 TTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAA 873
                                                                                                                                                                                                                                                                                               634 CCIGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAACCATTTTT 693
                                                                                                                                                                                                                                                               454 GTGGGCATGTCTCTGACCATCTGGACGGTGTGGGGGTCCTGTCACTATTTGGAGCTTTG 513
                                                                                                                                                                    514 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 573
                                                               334 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 393
                                                                                                             394 ACCATCATTGGAGCAGGAATCTTCATCTCCTAAGGGCGTGCTCCAGAACACGGGCAGC 453
                                                                                                                         874 GGTCAAACGCAGAACTITAAAGACGCCTTTICAGGAAGAGTTCAAGTATTACGCGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                694 ATTCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA
                                                                                                                                                                                                                                                   574 GAAGICITIGGICCATTACCAGCITTIGTACGAGICIGGGIGGAACICCICAIAAIACGC
                                                                                                                                                                                                                                                                                                                                                                                         754 GTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACC
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              Indels:
                                             US-09-667-170A-440 (1-2239) x ABB11957 (1-521)
                           Gaps:
    100.00%
63.66%
      Best Local Similarity:
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1354 ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCC 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
                                               1414 AGGIGGUITITIATIGGGCIGGCAGTIGCIGGGCTGAITIAICITCGAIACAAAIGCCCA 1473
                                                                                           1474 GATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGC 1533
                                                                                                                                       1534 CICTICAIGGIIGCCCTIICCCICIAIICGGACCCAIIIAGIACAGGGAIIGGCIICGIC 1593
                                                                                                                                                                                      1594 ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTATATGGGACAAGAAACCCAGG 1653
                                                                                                                                                                                                                                   1654 TGGTTTAGAATAATGTCAGAGAAATAACCAGAACATTACAAATAATACTGGAAGTTGTA 1713
               Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , blu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                tomato, monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; blodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                            Human EST encoded protein SEQ ID NO: 1439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 1001-1002; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian XB,
                                                                                                                                                                                                                                                                                                                                                      AAM23914 standard; Protein; 424 AA,
                                                                                                                                                                                                                                                                                  1714 CCAGAAGAAGATAAGTTA 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                               research use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-476164/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAH98573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200154477-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                    460 ATGTCTCTGACCATCTGGACGGTGTGGGGGTCCTGTCACTATTTGGAGCTTTGTCTTAT 519
                                                                                                                                                                                                                                                                                      520 GCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTC 579
                                                                                                                                                                                                                                                                                                                                          580 TITGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCA 639
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                                                                                                                                                                                                                                                                                                                                                         241 AlaValProIlePheValAlaLeuSerCysPheGlySerMetAsnGlyGlyValPheAla 260
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Mismatches:
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                                                                                                                                  424.00
100.008
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                                                       protein of the invention.
                                                                                 424 AA;
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s MJ, Mohamath R, Secrist H, Benson DR, Indirias CY;
Fling SP, Algate PA, Elliot M, Mannion J, Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lung tumour protein; immunostimulant; cytostatic; gene therapy; antisense-therapy; vaccine; immune response; lung cancer;
                                                                                                                                                                                                                                                                            1660 AGAATAATGTCAGAGAAAATAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAA 1719
                                                                                                                                       1480 CATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTC 1539
                                                                                                                                                                                    1540 AIGGITGCCCTITCCCTCIAITCGGACCCAITTAGTACAGGGAITGGCITCGICATCACI 1599
                                                                                                                                                                                                                                1600 CTGACTGGAGTCCCTGCGTATTATCTCTTTATTATGGGACAAGAAACCCAGGTGGTTT 1659
                                                                                          1420 CTITITATIGGGCIGGCAGIIGCIGGCIGAIITATCIICGAIACAAAIGCCCAGAIAI 1479
1300 ATTCATGTCCGCAAGCACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATG 1359
                                             1360 ATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGG 1419
                                                                                                                                                                                                                                                                                           New human lung-specific polynucleotides and polypeptides for the diagnosis and treatment of disease e.g. lung cancer ^{-}\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human T cell epitope related to lung tumour-specific protein.
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                                                                                                                                                                                                                                                                                                                                                                                                   AAE13851 standard; peptide; 16 AA.
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20000S-0640878.
20000S-234517P.
20000S-0704512.
2000US-0738973.
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                                                                                                                                                                                                                                                                                                                                1720 GAAGATAAGTTA 1731
                                                                                                                                                                                                                                                                                                                                                        421 GluAspLysLeu 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639201/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T cell epitope.
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22-SEP-2000;
01-NOV-2000;
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This represents a human amino acid permease homolog (AAPH). The AAPH nucleic acid, protein, AAPH (ant)agonists are useful in the diagnosis, treatment and prevention of cancer such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid or uterus; inflammatory/autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid permease homolog; AAPH; cancer; inflammatory disorder; AIDS; autoimmune disorder; anemia; asthma; atherosclerosis; diabetes mellitus; multiple sclerosis; osteoarthritis; osteoporosis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferation disorder; human.
                                                                        the development of cancer. The invention also relates to a composition useful for stimulating an immune response, and for treating cancer. The lung tumour specific oligonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence is human T cell epitope related to lung tumour-specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human amino acid permease homolog, useful in the diagnosis, treatment and prevention of cancer, inflammatory/autoimmune disorders and cell proliferation disorders -
The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and their antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition
                                                                                                                                                                                                                                                                                                                                                                                                   104 TICCAGGCCAAITGIGGCATAGATTITAICAIATICTGGATTITIGG 151
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY41159 standard; Protein; 511 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1A-F; 32pp; English.
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                                                                                                                                                                                            16 AA;
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generating hybridisation probes for mapping the naturally occurring

511 AA;

Sequence

Alignment Scores:

.. No

genomic sequence.

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disorders such as AIDS, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, astham, atheroscierosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, autoimmune hemolytic anemia, autoimmune mellitus, Crohn's disease, atopic dermatitis, dermatitis, diabetes emphysem, multiple scierosis, osteoarthritis, osteoporosis, rheumatoid arthritis, ulcerative colitis, viral, becterial, fungal, parasitic, protozoal infections; and cell proliferation disorders such as actinic, keratosis, cirrhosis, arteriosclerosis, myelofibrosis, and primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The protein can be expressed by standard recombinant methodology. AAPH polynucleotides and polypeptides are useful for diagnosis, treatment and prevention of cancer e.g. adenocarcinoma, lung cancer, ovarian cancer; inflammatory/autoimmune disorders e.g. ALDS, Crohn's disease, rheumatoid arthitis; and cell proliferation disorders e.g. arteriosclerosis, psoriasis, hepatitis. AAPH polynucleotides are useful in gene therapy, in PCR-based methods for detecting upstream sequences, and also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid permease homologue; AAPH; cancer; inflammatory disorder; autoimmune disorder; cell proliferation disorder; adenocarcinoma; AIDS; Crohn's disease; rheumatoid arthritis; arteriosclerosis; human; psoriasis; hepatitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human amino acid permease homologue (AAPH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human amino acid permease homolog (AAPH) polynucleotide and its complement useful for prevention and treatment of cancer, autoimmune
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corley NC, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-493508/41.
                                                                                                                                                                                            Sequence 511 AA;
                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                          thrombocythemia.
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DB:
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This invention describes a novel protein MONP-2 (I) and its encoding gene monp-2 (II) with a cell proliferation promoting effect isolated from a human peripheral blood. The new protein (I) and gene are useful in studying the expression abnormality and dysfunction of (I) as well as maintenance of immune function and development of drugs for e.g. immune diseases and cancers. This represents encodes the MONP-2 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel gene monp-2 encoding monocyte-specific protein with cell proliferation promoting effect, useful in studying its expression and immune function, and in developing drugs for e.g. immune diseases and
                                                                                                                                                                                                                                                                                     Human; monp-2; cell proliferation; drug development; immune disease;
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                        Conservative:
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                                       Mismatches:
                                                                                                           517 TATGCTGAATTGGGAACAACTATAAAGAAATCTGGA 552
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Indels:
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                                                                                                                                                                                   AAY87630 standard; Protein; 511 AA
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1.64%
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                                                                                                                                                                                                                                                              Human monp-2 protein.
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N-PSDB; AAA11954.
                   Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                 WO200017238-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoshimoto M,
                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                   01-AUG-2000
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                                               Query Match:
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                                                                                                                                                           RESULT
           Score:
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08 - SEP - 2000;

14 - SEP - 2000;

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16 - SEP - 2000;

17 - SEP - 2000;

18 - SEP - 2000;

19 - SEP - 2000;

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11 - SEP - 2000;

12 - SEP - 2000;

13 - SEP - 2000;

14 - SEP - 2000;

15 - SEP - 2000;

16 - SEP - 2000;

17 - SEP - 2000;

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02-OCT-2000;
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                                                                                                                                                                                                                                                                                                                              Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum.
                                                                                                                                                                                                                                                                                               Human digestive system antigen SEQ ID NO: 2514
                                                                 517 TATGCTGAATTGGGAACAACTATAAAGAAATCTGGA 552
                                                                                     US-09-667-170A-440 (1-2239) x AAY87630 (1-511)
                                                                                                                                                                                AAM93165 standard; Protein; 76 AA
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2000US-0218290.
2000US-0220963.
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2000US-0184664.
2000US-0186350.
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2000US-0190076.
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2000US-0209467.
2000US-0214886.
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2000US-0225758.
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2000US-0226279.
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2000US-0226868.
2000US-0227182.
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2000US-0217487.
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2000US-0225213.
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2000US-0225266.
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2000US-0225268
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2000US-0228924
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2000US-0229343
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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18 - AUG - 2000;
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06-SEP-2000;
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24-FEB-2000;
02-MAR-2000;
17-MAR-2000;
11-MAR-2000;
19-MAY-2000;
07-JUN-2000;
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23-AUG-2000;
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14-JUL-2000;
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2000US-0241787.
2000US-0241808.
2000US-0241809.
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2000US-0244617.
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2000US-0234274.
2000US-0234997.
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2000US-0231414.
2000US-0232080.
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2000US-0233063.
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2000US-0235836
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2000US-0241786
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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Sodium independent small neutral amino acid transporting proteins
                                                                                 (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                Claim 1; Page 62-65; 73pp; Japanese.
                                     09-JAN-2001; 2001WO-JP00031
                                                           07-FEB-2000; 2000JP-0028822
                                                                                                                          WPI; 2001-522461/57
                                                                                                      Kanai Y;
                                                                                                                                      N-PSDB; AAH74769
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                 16-AUG-2001
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                                                                                                      Endou H,
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      q
                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic collitis or ulcerative collitis. The present sequence is a digestive system antigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sodium independent small neutral amino acid transporter; cell resistance; oxidizing stress; NMDA type glutamate receptor; cell growth.
                                                                                                                                                                                                                                                                                                  Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a human amino acid transporter.
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Matches:
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                                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 2514; 986pp; English.
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                                                                                                                                                                                                                                                Ruben SM;
                                                     2000US-0249300.
2000US-0250160.
2000US-0250391.
                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                   2000US-0251988.
                       2000US-0249265
                                            2000US-0249299
                                                                                       2000US-0251030
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2000US-0251479.
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                                2000US-0249297
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                                                                                                                                                                                                                                                                  WPI; 2001-502630/55.
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 AA;
                                                                                                                                                                                                                                                                              N-PSDB; AAK88938
                              117 - NOV - 2000;
17 - NOV - 2000;
17 - NOV - 2000;
01 - DEC - 2000;
05 - DEC - 2000;
05 - DEC - 2000;
06 - DEC - 2000;
06 - DEC - 2000;
08 - DEC - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
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11-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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Sodium independent small neutral amino acid transporter; cell resistance; oxidizing stress; NMDA type glutamate receptor; cell {\sf growth}.
The present sequence represents a sodium independent small neutral amino acid transporter polypeptide. The polypeptides and polynucleotides are used for controlling cell resistance to oxidizing stress, NMDA type glutamate receptor activity, cell growth and for screening for substances that have these activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sodium independent small neutral amino acid transporting proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a murine amino acid transporter.
                                                                                                                                      523
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                              Gaps:
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                                                                                                                                                                                                                                                                                  57 GlyllePhelleSerProLysGlyValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 53-56; 73pp; Japanese
                                                                                                                                                                                                                                                                                                                                                      AAG63803 standard; Protein; 530 AA
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                                                                                         523 AA;
                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or egeptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, heematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activitianian activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
The present sequence represents a sodium independent small neutral amino acid transporter polypeptide. The polypeptides and polynucleotides are used for controlling cell resistance to oxidizing stress, NMDA type glutamate receptor activity, cell growth and for screening for substances that have these activities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 26487; 1399pp + Sequence Listing; English.
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                              63 GlyllePhelleSerProLysGlyValLeu 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 26487.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AA012595 standard; Protein; 43 AA
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10.00
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1.37$
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                                                                                                           530 AA;
                                                                                                                                                                                                                       Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAI92526
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                                                                                                                                                                                                    Percent Similarity:
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DB:
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019310) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 23421; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                        AA009529 standard; Protein; 62 AA.
                                                                                                                                                                                                                                                                                                     1 AspArgValSerLeuSerProArgLeu
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                               1.268
                                                                                                                          9.27
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                                                                        AA;
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                                                                                                                                                          Percent Similarity:
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                                                                        Seguence
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22-AUG-2000;
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                                                                                            Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and colypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome comparate chain reaction (PCR) primers, oligomers, and for chromosome comparation of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for restore normal activity of (II) is useful in gene therapy techniques considentifying expressed genes. (I) is useful in gene therapy techniques considentifying activity of (II) or to treat disease states involving considentiating a polypeptide in tissue, as molecular weight markers and as a molecular weight markers and as a magning of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. Calagnostics, foreniscs, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                        00000
                                                 Matches:
Conservative:
                                                                         Mismatches:
                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 50124; 103pp; English.
                                                                                                               US-09-667-170A-440 (1-2239) x AAO09529 (1-62)
                                                                                                                                                                                                                                                                             Novel human diagnostic protein #19756.
                                                                                                                                                   7 TrpHisAspLeuCysSerLeuGlnPro 15
                                                                                                                                     29 TGGCATGATCTCTGCTCACTTCAACCT 3
                                                                                                                                                                                                        ABG19765 standard; Protein; 87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C, Tang YT;
                                                          100.00%
100.00%
1.26%
22
                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217,
                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                       18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-639362/73.
                                                       Percent Similarity:
Best Local Similarity:
Query Match:
62 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS83952
                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
                     Alignment Scores:
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Seguence
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                                  No.:
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune/haematopoietic antigen SEQ ID NO:13520.
                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                          Matches:
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                                                                                                            Length:
                                                                                                                                                                                                         US-09-667-170A-440 (1-2239) x ABG19765 (1-87)
                                                                                                                                                                                                                                                       72 AAAAAGAAAGAAAGAAAAAAAGAGAGA 98
                                                                                                                                                                                                                                                                                                                             AAM85927 standard; Protein; 90 AA.
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2000US-0224519.
2000US-0225213.
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9.00
100.00%
100.00%
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2000US-0209467.
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2000US-0216647.
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20000S-0225759
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                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                           87 AA;
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                                                                                      Alignment Scores:
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19-MAY-2000;
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2000US-0246477.
2000US-0246478.
2000US-0246523.
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2000US-0246525.
2000US-0246526.
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2000US-0241826.
2000US-0244617.
22-AuG-2000; 2000US-0226868.
23-AuG-2000; 2000US-0227182.
23-AuG-2000; 2000US-0227182.
30-AuG-2000; 2000US-0228924.
01-SEP-2000; 2000US-0229345.
01-SEP-2000; 2000US-0229344.
01-SEP-2000; 2000US-0229345.
05-SEP-2000; 2000US-0229345.
06-SEP-2000; 2000US-0229345.
06-SEP-2000; 2000US-0231242.
08-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-0231413.
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2000US-0246528
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2000US-0246476.
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2000US-0241787
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2000US-0236368.
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2000US-0233065
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08-NOV-2000;
17-NOV-2000;
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20-OCT-2000;
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13-OCT-2000;
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02-OCT-2000;
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14-SEP-2000;
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14-SEP-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and proteins and polynucleotides may be used in the prevention, diagnosis and that affect they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome complement the patients own production of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (I) proteins and bolynucleotides may be used to prevent, proteins and polynucleotides may be used to prevent, concerns and cancer metastases of haematopoietic related disasses, especially cancers and cancer metastases of haematopoietic antigen genomic to AAK64703 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64942 to AAK64509 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Barash SC, Ruben SM;
17 - NOV - 2000; 2000US - 0249208.
17 - NOV - 2000; 2000US - 0249209.
17 - NOV - 2000; 2000US - 0249210.
17 - NOV - 2000; 2000US - 0249211.
17 - NOV - 2000; 2000US - 0249211.
17 - NOV - 2000; 2000US - 0249211.
17 - NOV - 2000; 2000US - 0249213.
17 - NOV - 2000; 2000US - 0249214.
17 - NOV - 2000; 2000US - 0249215.
17 - NOV - 2000; 2000US - 0249216.
17 - NOV - 2000; 2000US - 0249218.
17 - NOV - 2000; 2000US - 0249218.
17 - NOV - 2000; 2000US - 0249218.
17 - NOV - 2000; 2000US - 0249244.
17 - NOV - 2000; 2000US - 0249244.
17 - NOV - 2000; 2000US - 024929.
18 - DEC - 2000; 2000US - 024929.
05 - DEC - 2000; 2000US - 0251988.
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2000US-0251988.
2000US-0256719.
2000US-0251479.
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08-DEC-2000; 2000US-0251999.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-02540997.
05-JAN-2001; 2001US-0259678.
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08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868
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Length:
Matches:
Conservative:
Mismatches:
Indels:

8.32 9.00 100.00% 1.26% 22

90 AA;

Alignment Scores: Sequence

Percent Similarity: Best Local Similarity: Query Match: DB:

Gaps:

17 TrpHisAspLeuCysSerLeuGlnPro 25

AAY38429 standard; Protein; 132 AA.

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The inventoring tenders to mover number secreted polypeptides, and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells for use in treatment of a pathology related to aberrant expression or bysiological interactions of the polypeptides and cells agent to physiological interactions of the polypeptides and cells genetically or the nucleic acids encoding the polypeptides and cells genetically of the proteins are useful in genetic vaccination, testing and consequences them are also useful for producing the polypeptides of cells genetically the proteins are useful in genetic vaccination, testing and consequences tendon as nutritional supplements. They may be used to bone, cartilage, tendon and/or nerve tissue growth or regeneration; cimmune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU39510-AAU33304 represent the amino acid over the consequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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US-09-667-170A-440 (1-2239) x AAM85927 (1-90)
                                                                                                                           49 TrpHisAspLeuCysSerLeuGlnPro 57
                                                                             29 TGGCATGATCTCTGCTCACTTCAACCT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human secreted protein #2255.
                                                                                                                                                                                                                                                                                             AAU31764 standard; Protein; 119 AA.
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26-JAN-2001; 2001US-0770160.
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                                                                                                                                                                                                                           RESULT 14
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AX B X B X B

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma: lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AlDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; esteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Human secreted protein encoded by gene No. 32.

30-SEP-1999 (first entry)

AAY38429;

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This sequence represents a secreted human protein encoded by the gene fusion perceins by linking to the gene to a human immunoglobulin Feroreins by linking to the gene to a human immunoglobulin Feroreins by linking to the gene to a human immunoglobulin Ferorein as compared to the human protein only.

The invention relates to 36 novel genes and their fragments (nucleic which are useful for preventing, treating or ameliorating medical sequences. AAZ06219-206263; amino acid sequences AAX08386-738498) conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 36 year haznézia for heavel the new polynucleotides. Specific uses are described for each of the 36 year haznézia for highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 202-203; 227pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.23%
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-444190/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ06262
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```

Conservative: Mismatches: Length: Matches:

100.00% 100.00% 1.26%

Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

Indels:

US-09-667-170A-440 (1-2239) x AAU31764 (1-119)

29 TGGCATGATCTCTGCTCACTTCAACCT 3

Ni J;

DW,

Lafleur Soppet

Ebner R, Ruben SM,

Duan RD, Rosen CA,

Brewer LA, Olsen HS,

(HUMA-) HUMAN GENOME SCI INC.

99WO-US00108. 98US-0070704. 98US-0070692. 98US-0070657.

06-JAN-1999;

15-JUL-1999

07-JAN-1998; 07-JAN-1998; 07-JAN-1998;

Homo sapiens. WO9935158-A1.

Search completed: April 16, 2003, 16:35:36 Job time : 77.5 secs

```
Command line parameters:

**MODEL=frame+_n2p.model -DEV=x1h

**O=cgn2_LVGFPC_spool_UVG09667170/runat_04042003_091002_21212/app_query.fasta_1.2375

**O=FGG072_LVGFPC_spool_UVG09667170/runat_040476-01 -LoOPCL=0 -LOOPCL
                                                                                                                                                                                                                                                                                                                                                                                                                   (without alignments)
9896.320 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     April 16, 2003, 16:29:36 ; Search time 43.5 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Egapop 6.0 , Egapext 7.0 Delop 6.0 , Delext 7.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                   Run on:
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1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*
Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description Coat protein - phanish and protein major coat protein B of conserved hypothet transcription fact AtHVA22, 5056-49 fapR protein - Eschypothetical protein protein protein protein and protein prot	related to homeoti
1	T51078
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	7
Ouery Match Length DB 1.1 46 1 1.1 67 2 1.1 82 2 1.1 100 2 1.1 159 2 1.1 159 2 1.1 287 2 1.1 287 2 1.1 359 2	361
Ouery Match	1.1
0 0 	ю
Result No. 1 2 3 3 4 6 C 7 C 10 10 11 13	4

hypothetical prote hypothetical prote unknown protein (i homeotic protein (i hypothetical prote hypothetical prote hypothetical prote F6A4.19 protein - probable Ste20-11k	leucyl aminopeptid leucine aminopepti aldehyde dehydroge LATI protein - hum probable aldehyde hypothetical prote hypothetical prote		hypothetical prote penicillin-binding cardiac morphogene hypothetical prote genome polyprotein extensin homolog T mammary gland fact mammary gland fact
4447 1133 1133 1133 1133	G86538 G72083 AC3043 JG0165 J27612 T27612	131534 137665 1376282 116854 123624 123624	312 312 716 506 506 529 777
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ALIGNMENTS

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C.Species: phage pil
C.Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 31-Dec-1993
C.Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 31-Dec-1993
R.Nakashima, Y.: Wiseman, R.L.; Konigsberg, W.; Marvin, D.A.
Nature 253, 68-71, 1975
A.Title: Primary structure and sidechain interactions of PFL filamentous bacterial vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tibosomal protein S21 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Bate: 08-May-1998 #sequence_revision 08-May-1998 #text_change 13-Aug-1999
C;Accession: A70375
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                           A/Residues: 1-46 <NAX>
C;Comment: Pfl is a filamentous bacteriophage with single-stranded DNA.
C;Superfamily: filamentous phage coat protein B
                                                                                                                                                                                                                                                                                                                                           8
0
0
0
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1432 CTGGCAGTTGCTGGGCTGATTAT 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 100.008
Best Local Similarity: 100.008
Query Match: 1.098
                                                                                                                                                                                                                                                                                                                                                    8.00
                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-46 <NAK>
coat protein - phage Pfl
                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                      Pred. No.:
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A; Rolecule type: DNA
A; Residues: 1-100
CKUR>
A; Cross references: GB:AE006469; PIDN:AAK64834.1; PID:g14523247; GSPDB:GN00165
A; Cross references: GB:AE006469; PIDN:AAK64834.1; PID:g14523247; GSPDB:GN0165
A; Experimental source: strain 1021, megaplasmid pSymA
A; Experimental source: S.R.; Long, S.R.; Publier, A; Abola, P.; Ampe, F.; Barloy-Hubl
E; Annan, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
A; Authors: Kahn, D.; Vandehol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Actitle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein SMa0325 [imported] - Sinorhizobium meliloti (strain 10 C;Species: Sinorhizobium meliloti (c;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                               A;Cross-references: GB:AE004507; GB:AE004091; NID:99946596; PIDN:AAG04112.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein slr0921 - Synechocystis sp. (strain PCC 6803)
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                                                                                                                                                                         C;Superfamily: filamentous phage coat protein B
                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-667-170A-440 (1-2239) x H95283 (1-100)
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-667-170A-440 (1-2239) x C83556 (1-82)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1075 CTGACAAATGTGGCCTACTTTACG 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1432 CIGGCAGTIGCTGGGCTGATITAT 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 LeuAlaValAlaGlyLeuIleTyr 76
                                                                                                         A, Experimental source: strain PAO1
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                                                                                                                                                                                                                                                51.8
8.00
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                                            A; Molecule type: DNA
A; Residues: 1-82 <STO>
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                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: H95283
                                                                                                                                                          coaB; PA0723
                                                                                                                                                                                                                                                                                                   Percent Similarity:
A; Accession: C83556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Genome: plasmid
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                                                                                                                                              C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coat protein B of bacteriophage (Pfl) PA0723 [imported] - Pseudomonas aeruginosa (strain c'Species: Pseudomonas aeruginosa (species: Pseudomonas aeruginosa PA01, M.J.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Licky, M.J.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.

"Icry, S.; Olson, M.V.

"Icry, S.; Olson, M.V.

"Intle: Complete genome sequence of pseudomonas aeruginosa PA01, an opportunistic pathor A; Reference number: A882950; MUID: 20437337; PMID: 10984043
                                                                                                                                                               A,Cross-references: GB:AE000711; NID:g2983401; PIDN:AAC06990.1; PID:g2983406; GB:AE00065
A,Experimental source: strain VF5
                   Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Recession: A70375
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-67 <AQF?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         major coat protein precursor - phage Pf1
M.Alternate names: gene 8 protein
C;Species: phage Pf1
C;Species: phage Pf1
C;Species: phage Pf1
C;Species: phage Pf1
C;Accession: S15143; S20699
R;Hill, D.F.; Short, N.J.; Perham, R.N.; Petersen, G.B.
J. Mol. Biol. 218, 349-364, 1991
A;Mitle: DNA sequence of the filamentous bacteriophage Pf1.
A;Reference number: S15140; MUID:91186399; PMID:2010913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:X52107; NID:914829; PIDN:CAA36331.1; PID:914833
A;Experimental source: ATCC 25102-B1
C;Superfamily: filamentous phage coat protein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1-36/Domain: signal sequence *status predicted <SIG>F;37-82/Product: major coat protein *status predicted <WAT>
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Conservative:
Mismatches:
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Mismatches:
Indels:
                                                                                                                                                                                                                                                  A;Gene: rpsU
C;Superfamily: Escherichia coli ribosomal protein S21
                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-667-170A-440 (1-2239) x A70375 (1-67)
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Query Match:
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A; Residues: 1-82 <JMO>
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                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, J.; Sakano, H. Liu, Z.A.; Lutos, J.S.; Maiti, R.; Marzia A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A.Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Reference number: A86141; MUID: 21016719; PMID: 11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Not. Microbiol. 4, 1779-1783, 1990
A) File: Characterization of FapR, a positive regulator of expression of the 987P open A). Reference number: S11984; MUID:91171879; PMID:2077360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-260 <KLA>
A;Cross-references: EMBL:X53494
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in lacking 96.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                             A) Cross-references: GB: AE005173; NID: 96665546; PIDN: AAF22915.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S11984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PAB0790 - Pyrococcus abyssi (strain Orsay)
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Mismatches:
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C.Superfamily: fapR protein
C.Keywords: DNA binding; transcription regulation
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                                      F.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                               A;Cross-references: EMBL:D64003; GB:AB001339; NID:91001200; PIDN:BAA10472.1; PID:9100123
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr0921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Accession: T05279
R.Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De ewes, H.W.; Mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database, September 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: tobacco DNA-binding protein tbz17; fos/jun DNA-binding domain homology
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S75737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription factor ATB2 - Arabidopsis thaliana
N.Alternate names: protein 14L20.170
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 33-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                              A; Status: nucleic acid sequence not shown; translation not shown
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A.Cross-references: EMBL.AL023094
A.Experimental source: cultivar Columbia; BAC clone T4L20
                                                                                                                                                   A; Reference number: S74322; MUID:97061201; PMID:8905231
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related to homeotic protein Antennapedia [imported] - Neurospora crassa N.Alternate names: protein B2A19.120 C. Species: Neurospora crassa C. Species: Neurospora crassa C. Species: 11-011.2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C. Accession: T51078 R. Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, July 2000 A; Reference number: Z25286 A; Accession: T51078
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DNA Cell Biol. 13, 857-863, 1994
A; Title: Molecular cloning of a chick cochlea cDNA encoding a subunit of DNA replicat
A; Reference number: I50704; MUID: 94347215; PMID: 8068208
A; Accession: I50704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replication factor C/activator 1 subunit - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999.
C;Accession: I50704
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A;Molecule typim:lanA
A;Residues: 1-361 <SCH>
A;Residues: 1-361 <SCH>
A;Cross-references: EMBL:AL390092; GSPDB:GN00116; NCSP:B2A19.120
A;Experimental source: BAC clone B2A19; strain OR74A
C;Genetics:
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A;Cross-references: GDB:283460
A;Map position: 7q11.23-7q11.23
C;Superfamily: phage T4 DNA polymerase accessory protein 44
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Pred. No.:
Score:
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Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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A; Residues: 1-353 <CHE>
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                                     A;Status: preliminary
A; Accession: A42700
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Roc. Natl. Acad. Sci. U.S.A. 89, 2516-2520, 1992
A; Title: Sequence and expression in Escherichia coli of the 40-kDa subunit of activator A; Reference number: A42700; MUID:92212860; PMID:1313560
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A, Reference number: A62870
A, Accession: B82933
A, Accession: B82933
A, Status: preliminary
A, Wolecule type: DNA
A, Residues: 1-348 <GLA>
A, Residues: 1-348 <GLA
A, Residues: 1
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C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 16-Aug-2002
C; Accession: E82933
F; Glass, J.I.: Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to GenBank, February 2000
A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
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                                                                                                                        A, Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A, Reference number: A75001
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C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Aug-1998
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                                                                                           R; anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-667-170A-440 (1-2239) x H75098 (1-287)
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-366 <WIL)-
A;Cross references: EMBL:AL032630; PIDN:CAA21558.1; GSPDB:GN00028; CESP:Y62H9A.1
A;Experimental source: clone Y62H9A
A;Gene: CESP:Y62H9A.1
                                                                                                                                                                                                                                                                                            hypothetical protein Y62H9A.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
R;Steward, C.
Submitted to the EMBL Data Library, October 1998
A;Reference number: 220334
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A;Introns: 25/3; 206/3; 287/2; 342/1
                                                                          Pred. No.: 44.5
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.09%
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A; Gene: NCSP:B2A19.120
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A;Introns: 282/2
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-0-/cgn2_1/USPTC_spool/US09667170/runat_04042003_091001_21192/app_query.fasta_1.2375  
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-0-/cgn2_1/USPTC_spool/US09667170/runat_01n2p_rsp - MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 - UNITS=bits -START=1 - END=-1 - MATRIX=0.0190 - TRANS=human40.cdi  
-UST=45 - DOCALIGN=200 -THR_SCORE=quality - THR_MIN=1 - ALGN=15 - MODE=LOCAL  
-UST=45 - DOCALIGN=200 - THR_SCORE=quality - THR_MIN=1 - ALGN=15 - MODE=LOCAL  
-USER=US09667170_cGCN_1_1_24_eruat_c04042003_.091001_21192 - NCPU=6 - TCPU=3  
-NO_XLPXY - NO_MAAP - LARGEQUERY - NEC_SCORES=0 - WAIT - LONGLOG - DEV_TIMEOUT=120  
-WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=60 - XGAPEXT=60 - FCAPOP=6 - FCAPEEXT=7  
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Copyright (c) 1993 - 2003 Compugen Ltd.
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RECN. RICPR ST5B_MOUSE ST5B_MOUSE ST5A_RAT ST5A_RAT SSS1_YEAST UFD4_YEAST POLG_HPAV2 POLG_HPAV2 POLG_HPAV2 POLG_HPAV2 VO48_BORBU C552_BRAJA C552_BRAJA SECE_ECOLI SECE_ECOLI RS9_CHTRR	INIZ_PANTR RS9_CHLMU SECR_MOUSE RS9_CHLPN ATPE_SYNY3 X_WHV1		Chordata; Craniata; v Primates; Catarrhini; ubMed-11213471; Kuriyama-Matsumura K., and expression of huma t system xc; gnal. 2:665-671(2000).	chain implicated he EMBL/GenBank/ ang H., Huang W. regulation of hun gment epithelial he EMBL/GenBank/I alacin M., Pinede
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		ST/ (Rel. (Rel. (Rel. (Rel. tamate	mns (Human) Metazoa; Eutheria; =9606; ROM N.A. 082210; Pu amba M., K cloning a transport Redox. Sig	FROM N.A. S., Beach D. Ovel CD98 11s; "" (NOV-1999) t FROM N.A. Toch I.A. To
888888888888888888888888888888888888888	, , , , , , , , , , , , , , , , , , , ,	LUMAN XCT-HUMAN STANI Q9UPYS; 16-OCT-2001 (Rel. 4/ 16-OCT-2002 (Rel. 4/ Cystine/glutamate tr (Calcium channel blc SLC7All.	Homo sapiens (Human). Bukaryota: Metazoa; Chordata; Cran Mammalia: Eutheria: Primates; Cata NCBI_TaxID=966; [1] SEQUENCE FROM N.A. MEDLINE=21082210; PubMed=11213471; Sato H., Tamba M., Kuriyama-Matsum "Molecular cloning and expression amino acid transport system xc."; Antioxid. Redox. Signal. 2:665-671	CORNIID D.S., Beach "CCBRI, novel CD98 1 signaling "; Submitted (NOV-1999) [3] EDGENCE FROM N.A. TISSUE-Placenta, Chancy C.D., Kekuda I Chancy C.D., Kekuda I Structure, function "Structure, function transporter in reting Submitted (APR-2000) [4] EDGENCE FROM N.A. BOTSANI G., MANZONI SEQUENCE FROM N.A. SIDMITTED (JAN-2002) [5]
119 20 20 20 20 20 20 20 20 20 20 20 20 20	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	LT 1 HUMAN XCT_1 Q9UP) 16-00 16-00 15-JU Cystj (Calc	Hom Euk Mam NCB [1] SEQ SEQ MED Sat "Mo ami	SEQ SEQ SEQ SUB SUB SEQ CCAN TIS SEQ SUB SEQ SEQ ([4]
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                                                                                                                                                                                                                                   PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- PUNCTTON: SODIUM.INDEPENDENT, HIGH-AFFINITY EXCHANGE OF ANIONIC
AMINO ACIDS WITH HIGH SPECIFICITY FOR ANIONIC FORM OF CYSTINE AND GLUTAMATE (BY SIMILARITY).
-!- SUBUNIT: DISULETIDE-LINKED HETERODIMER WITH THE AMINO ACID
TRANSPORT PROTEIN SLG3AZ/AF2HC (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 GluLysValGlnLeuLysArgLysValThrLeuLeuArgGlyValSerIleIleIleIly 55
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InterPro; IPR002293; AA/rel_prmeasel
InterPro; IPR004760; L_AA_transport.
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TIGRFAMS; TIGR00911; 2A0308; 1.
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EMBL, AF200708; AAG35592.1; --
EMBL, AF228972; AAK49111.1; --
EMBL, AJ277882; CAC81905.1; --
EMBL, BC012087; AAH12087.1; --
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACID TRANSPORT PROTEIN SIC3A2/4F2HC.
SUBCELLULAR LOCATION: Integral membrane protein (Probable).
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cystine/glutamate transporter (Amino acid transport system xc-) (xCT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-129/SvJ; TISSUE-Liver;
Sasaki H., Sato H., Bannai S.;
"Isolation and functional characterization of mouse cystine/glutamate exchange transporter gene.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY EXCHANGE OF ANIONIC
AMINO ACIDS WITH HIGH SPECIFICITY FOR ANIONIC FORM OF CYSTINE AND
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99223452; PubMed=10206947; Sato H., Tamba M., Ishli T., Bannai S.; "Cloning and expression of a plasma membrane cystine/glutamate exchange transporter composed of two distinct proteins."; J. Biol. Chem. 274:11455-11458(1999).
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TIGRFAMS; TIGR00911; 2A0308; 1.
Transport; Amino-acid transport; Transmembrane.
TRANSMEM 44 64
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InterPro; IPR002293; AA/rel_prmeasel
InterPro; IPR004760; L_AA_transport.
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EMBL; AB037660; BAA90522.1; JOINED.
                                                      1714 CCAGAAGAAGATAAGTTA 1731
                                                                                       496 ProGluGluAspLysLeu 501
                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                (Mouse).
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Q9WTR6;
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1171 TTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGT 1230
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"Identification and characterization of a membrane protein (y+L amino acid transporter-1) that associates with 4F2hc to encode the amino acid transport activity y+L. A candidate gene for lysinuric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 PheSerLeuAlaValProIlePheValAlaLeuSerCysPheGlySerMetAsnGlyGly 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09UM01; 09P2V5; 095984; [1.6.cort-2001 (Rel. 40, Created)] [1.6.cort-2001 (Rel. 40, Last sequence update)] [1.6.cort-2001 (Rel. 40, Last sequence update)] [1.6.cort-2001 (Rel. 41, Last annotation update)] [1.6.cort-2002 (Rel. 41, Last annotation update)] [1.6.cort-2003 (Rel. 41, Last annotation 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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MEDLINE-99047611; PubMed=9829974;
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TISSUE=Placenta;

EMBL outstation

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between the Swiss Institute of Bioinformatics and the
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SUBCELLULAR LOCATION: Integral membrane protein (Probable).

TISSUE SPECIFICITY: EXPRESSED IN KIDNEY >> PERIPHERAL BLOOD
LEUKOCYTES >> LUNG >> PLACENTA = SPLEEN >> SMALL INTEGRINE.

DISEASE: DEFECTS IN SIC7A7 ARE A CAUSE OF IXSINIBLE PROTEIN
INTOLERANCE (LPI). LPI IS AN AUTOSOMAL RECESSIVE MULTISYSTEM
DISORDER FOUND MATINI: IN FINIAND AND ITALY. ON A NORMAL DIET, LPI
PATIENTS PRESENT POOR FEEDING, VOMITING, DIARRHEA, EPISODES OF
HYPERAMMONIABMIC COMA AND GROWTH RETARDATION. HERATOSPLENOMEGALY,
OSTEODOROSIS AND A LIFE-THREATENING PULMONARY INVOLVERENT
(ALVEOLAR PROTEINOSIS) ARE ALSO SEEN. BIOCHEMICALLY LPI IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mykkaenen J., Torrents D., Pineda M., Camps M., Yoldi M.E.,
Horelli-Kuitunen N., Huoponen K., Heinonen M., Oksanen J., Simell O.,
Savontaus M.-L., Zorzano A., Palacin M., Aula P.;
"Functional nallysis of novel mutations in y+LAT-1 amino acid
transporter gene causing lysinuric protein intolerance (LPI).";
Hum. Mol. Genet. 9:431-438(2000).
                Borsani G., Bassi M.T., Sperandeo M.P., De Grandi A., Buoninconti A.,
Riboni M., Manzoni M., Incerti B., Pepe A., Andria G., Ballabio A.,
                                                                                                                                                                                                                                                                                                                                                                                                      TEXPENCE FROM N.A.
Takayama K., Yoshimoto M.;
"Molecular and biological characterization of a novel monocyte amino
                                                                      "SLC7A7, encoding a putative permease-related protein, is mutated in
                                                                                                                                                                                                                                                                MEDLINE-20202143; PubMed-10737982; Moguchi A., Shoji Y., Molauni A., Takahashi T., Shoji Y., Malsawa S., Matsumori M., Kayo T., Obata T., Wada Y., Yoshimura I., Maisawa S., Konishi M., Takasago Y., Takada G.; Takada G.; SizChAA genomic structure and novel variants in three Japanese Issurant protein intolerance families."; Hum. Mutat. 15:367-372(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20100611; PubMed=10631139; Sperandeo M.P., Bassi M.T., Riboni M., Parenti G., Buoninconti A., Sperandeo M.P., Bassi M.T., Riboni M., Parenti G., Strisciuglio P., Dianzani I., Parini R., Candito M., Endo F., Ballabio A., Andria G., Sebastio G., Borsani G.; afterce of the SLC7A7 gene and mutational analysis of patients affected by lysinuric protein intolerance."; Am. J. Hum. Genet. 66:92-99(2000).
                                                                                                                                                                           Fukasawa Y., Segawa H., Endou H., Kanai Y.; "Characterization of a human system y+L amino acid transporters."; Submitted (NoV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZED BY A DEFECT IN THE PLASMA MEMBRANE TRANSPORT OF DIBBASIC AMINO ACIDS.
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SUBUNIT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid permease, MOP-2.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                      patients with lysinuric protein intolerance.";
Nat. Genet. 21:297-301(1999).
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 MEDLINE=99178268; PubMed=10080183;
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                                                                                                                                                          TISSUE=Kidney;
                                                   Sebastio G.;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Disease mutation.
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S -> R (IN LPI).
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L -> R (IN LPI).
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G -> D (IN LPI).
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InterPro; IPR004841; Permease.
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30-MAY-2000 (Rel. 39, Created)
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55990 MW;
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BC010107; AAH10107.1;
HGNC:11065; SLC7A7.
                                                                                                  AJ130718; CAA10198.1;
AF092032; AAC83706.1;
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Best Local Similarity:
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AB031534;
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AB031536;
AB011263;
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AC 067028;
DT 30-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                    Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V., "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                      Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
                                                                                                                                                                                                                                             Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hill D.F., Short N.J., Perham R.M., Petersen G.B.;
"DNA sequence of the filamentous bacteriophage Pfl.";
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Mismatches:
30-WAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 30S ribosomal protein S21. RPSU OR AQ_867 OR AQ_867A.
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001911; Ribosomal_S21.
PRAM: PF01165; Ribosomal_S21; 1.
PRINTS: PR00976; RIBOSOMALS21.
PRODOM: P0005521; Ribosomal_S21; 1.
PROSTIE; PS01181; RIBOSOMAL_S21; 1.
PROSTIE; PS01181; RIBOSOMAL_S21; FALSE_NEG.
Ribosomal protein; Complete protecome.
SEQUENCE 67 AA; 8261 MW; E1897087A487EF70
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01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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NCBI_TaxID=10871;
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                                                                                                                                                     MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 GAAAGAAAGAAAAGAGAGAGG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-AICC 25102-B1;
MEDLINE-91186399; PubMed-2010913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 GluArgLysLysLysArgGluArg 50
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000711; AAC06990.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.00
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                    NCBI_TaxID=63363;
                                                          Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage Pf1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 37-82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                        -!- FUNCTION: COAT PROTEIN B IS THE MAJOR COAT PROTEIN OF THE VIRION.
                                                                                                                                                                                STRUCTURE BY NMR.
MEDLINE=92022521; PubMed=1925543;
Nambudripad R., Stark W., Opella S.J., Makowski L.;
"Membrane-mediated assembly of filamentous bacteriophage Pfl coat
            Nakashima Y., Wiseman R.L., Konigsberg W., Marvin D.A.; Primary structure and sidechain interactions of Pfl filamentous
                                                                                                                        "Pfl virus structure: helical coat protein and DNA with paraxial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
987P fimbrial operon positive regulatory protein fapR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E -> Q (IN REF. 2).
25FD055DA4661504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-667-170A-440 (1-2239) x COAB_BPPF1 (1-82)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
 MEDLINE=75082355; PubMed=1110754;
                                                                                               MEDLINE=94310463; PubMed=8036516;
Liu D.J., Day L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1432 CTGGCAGTTGCTGGGCTGATTTAT 1455
                                          virus coat protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 LeuAlaValAlaGlyLeulleTyr 76
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X52107; CAA3631.1; PIR; A04229; VCBPPF. PIR; S15143; S15143. PIR S20699; PDB; IIFM; 31 JUL-94. PDB; IIFM; 31 JUL-94. PDB; ZIFM; 01 JAN-96. PDB; ZIFM; 01 JAN-96.
                                                                                                                                                                                                                                                         Science 252:1305-1308(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
82
55
78
82
45
8377 MW;
                                                                                                                                                   Science 265:671-674(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.008
100.008
1.098
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                                                      Nature 253:68-71(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coat protein; Signal;
SIGNAL 1 36
CHAIN 37 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity;
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                                                                                                                                           phosphates.
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P23774;
                                                                                                                                                                                                                                             protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match:
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FAPR_ECOLI
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Hurwitz J.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-92212860; PubMed-1313560;
Chen M., Pan Z.-Q., Hurwitz J.;
"Sequence and expression in Escherichia coli of the 40-kDa subunit of
activator 1 (replication factor C) of HeLa cells.";
Proc. Natl. Acad. Sci. U.S.A. 89:2516-2520(1992).
                                                                                                            P35250; P32846;
01-FEB-1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Activator 1 40 kDa subunit (Replication factor C 40 kDa subunit) (Al
40 kDa subunit) (RF-C 40 kDa subunit) (RFC40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PSO0041; HTH_ARAC_FAMILY_1; 1.
PROSITE; PSO1124; HTH_ARAC_FAMILY_2: 1.
Transcription regulation; DNA-binding: Activator.
DNA_BIND 170
DNA_BIND 170
SEQUENCE 260 AA; 30349 MW; 1F73401737062C7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 232-249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-667-170A-440 (1-2239) x FAPR_ECOLI (1-260)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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MEDLINE=91171879; Pubmed=2077360;
                                                                                                                                                                                                                                                                                                                                                                           PIR; S11984; S11984.
InterPro; IPR000005; HTHARAC.
Pfam; PF00165; HTH_ARAC; 2.
PRINTS; PR00032; HTHARAC.
SMART; SM00342; HTH_ARAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 189 F
260 AA; 30349 MW;
                                                                                                                                                                                                                                                                                                                                                              EMBL; X53494; CAA37578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
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8.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
           Escherichia coli
                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                 REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC14_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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          Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: THE ELONGATION OF PRIMED DNA TEMPLATES BY DNA POLYMERASE
-!- FUNCTION: THE ELONGATION REQUIRES THE ACTION OF THE ACCESSORY PROTEINS
PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) AND ACTIVATOR 1. THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                      40 kba SUBBUNIT BINDS ATP.

-1- SUBBUNIT BINDS ATP.

-1- SUBBUNIT HETEROPENTAMER OF SUBBUNITS OF 140/145, 40, 38, 37, AND 36.5 kba THAT FORMS A COMPLEX WITH PCNA IN THE PRESENCE OF ATP.

-1- SUBCELLULAR LOCATION: Nuclear (Probable).

-1- DISEASE: Haploinsufficiency of RFC2 may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in williams. Beuren syndrome (WBS), a rare developmental disorder. It is a contiguous gene deletion syndrome involving genes from chromosome band 7911.23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Activator 1 40 kDa subunit (Replication factor C 40 kDa subunit) (Al 40 kDa subunit) (RF-C 40 kDa subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE ACTIVATOR 1 36 TO 40 kDa SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G -> L (IN REF. 1; AA SEQUENCE).
B50AC8EEF89F64A9 CRC64;
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SMART; SM00382; AAA; 1.
DNA replication; ATP-binding; Nuclear protein;
Williams-Beuren syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-667-170A-440 (1-2239) x AC14_HUMAN (1-354)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR000862; RFCdomain.
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354 AA; 39157 MW;
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SEQUENCE FROM N.A.
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                                                                                           Oberholtzer J., Cohen E.L., Davis J.G.;
"Molecular cloning of a chick cochlea cDNA encoding a subunit of DNA replication factor (Zactivator 1.";
DNA Cell Biol. 13:857-863(1994).
-!- FUNCTION: THE ELONGATION OF PRIMED DNA TEMPLATES BY DNA POLYMERASE DELTA AND EPSILON REQUIRES THE ACTION OF THE ACCESSORY PROTEINS PROLIFERATING CELL NUCLEAR ANTIGEN (PONA) AND ACTIVATOR 1. THE
                                                                                                                                                                                                             40 KDA SUBUNIT BINDS ATP (BY SIMILARITY)'
-!- SUBUNIT: HETEROPENTAMER OF SUBUNITS OF 140/145, 40, 38, 37, AND
36.5 KDA THAT FORMS A COMPLEX WITH PCNA IN THE PRESENCE OF ATP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: BELONGS TO THE ACTIVATOR 1 36 TO 40 kDa SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goriely A., Stella M., Coffinier C., Kessler D., Mailhos C., Dessain S., Desplan C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IP (POTENTIAL)
A2FD38F964CD11F9 CRC64;
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00382; AAA; 1.
DNA replication; ATP-binding; Nuclear protein.
81 88 APP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P54366, Q9VPR9,
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-667-170A-440 (1-2239) x AC14_CHICK (1-359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003593; AAA ATPase.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR000862; RFCdomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                 STRAIN-Leghorn; TISSUE-Cochlea;
MEDLINE-94347215; PubMed-8068208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1761 CTGCCCAAGGGGAGACACAAATA 1784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Embryo;
MEDLINE=96202483; PubMed=8625850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 359 AA; 39706 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U12438; AAA20552.1; -
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100.00%
1.09%
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GSC OR CG2851,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.4
8.00
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                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                   FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSC_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
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RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addms M.D., Celniker S.E., Holt R.A., Fashurner M., Henderson S.N.,
RA Addms M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Gocage R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baladyin D.,
Ballew R.M. Basu A., Baxendale J., Baytaktaroglu L., Beasley E.M.,
Beeson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berins D. Butler H., Cadleu E., Center A., Chadra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chadra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Gord K., Gong F. Gorfell J.H., Gu Z., Gabart W.M., Glasser K.,
RA Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wein M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lu X., Mattel B.W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Hostin D. R., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Hoston D.R., Moy M., Murphy B., Murphy L., Wardy S., Suh H. Y.,
Randert K., Siden-Klamos I., Simpson M., Stupski M.P., Smith T.,
RA Hard R., Technik R., Venter R., Venter B., Yen G., Yan G., Yan G., Yan G., Yan R.,
Rand B.C., Siden-Klamos I., Simpson M., Stupski M. P., Smith H.,
Ray B. Hoston R.A., Welnistock G.M., Weissenbach J.,
Ray Hang Z.-Y., Wassarman D.A., Weiter J., Ray Gibbs R.A., Woodege T., Worley L., Sung G., Zhan M., Zhang G., Zhan M., Shang G., Zhan M., Zhang G., Zhan K., Shang G., Zhan K., Shang G., Zhang G., Zhang G., Zhang G., Zhang G., Shang G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang G., Zha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: IN EARLY EMBRYO DEVELOPMENT, EXPRESSION CONFINED TO TWO REGIONS: A HORSESHOB-LIKE PATTERN ACROSS THE DORSAL SIDE WHICH IS DESTINED TO FORM THE BRAIN HEALSPHERES AND A SECOND DOMAIN WHICH INVACINATES INSIDE THE STOMODEUM AND WHICH, IS PATED TO FORM THE FOREGUT, RING GLAND AND STOMATOGASTRIC NERVOUS
                                                                    SEQUENCE FROM N.A.
MEDLINE-96272167; PubMed-8670808;
Hahn M., Jackle H.;
"Drosophila goosecoid participates in neural development but not in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "BICOID" SUBFAMILY.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: APPEARS TO REGULATE REGIONAL DEVELOPMENT OF SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUES. CAN RESCUE AXIS POLARITY IN UV-RADIATED XENOPUS
"A functional homologue of goosecoid in Drosophila."; Development 122:1641-1650(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                   body axis formation.";
EMBO J. 15:3077-3084(1996).
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM (SNS).
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TISSUE-Fetal retina;
MEDLINE-96276417; PubMed-8694763;
Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I.,
Merlevede W., Goris J., Hemmings B.A.;
"The variable subunit associated with protein phosphatase 2A0 defines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
epsilon isoform (PP2A, B subunit, B' epsilon isoform) (PP2A, B
subunit, B56 epsilon isoform) (PP2A, B subunit, PR61 epsilon isoform)
(PP2A, B subunit, R5 epsilon isoform).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPARTMENT:
SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                               protein; Nuclear protein; DNA-binding; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                         851A4C46AA861FB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a novel multimember family of regulatory subunits."; Biochem. J. 317:187-194(1996).
                                                                                                                                                                                                                                                419
8
0
0
0
0
                                                                                                                                                                                                                                                                         Conservative:
                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                          467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 449-455
                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                       US-09-667-170A-440 (1-2239) x GSC_DROME (1-419)
                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                            POLY-ALA.
POLY-SER.
                                                                                                                                                                                   POLY-ALA.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                               1724 TCTTCTTCTGGTACAACTTCCAGT 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISSUE=Fetal brain;
MEDLINE=96355607; Pubmed=8703017;
                                                                                                                                                                                                                                                                                                                                                                              370 SerSerSerGlyThrThrSerSer 377
                                                                                                      SMART: SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                           TRANSFAC; T04041; -. FlyBase; FBgn0010323; Gsc. InterPro; IPR001356; Homeobox.
                                                                                                                                                                                 195 199 PO 286 345 H
                                                                                  Pfam; PF00046; homeobox; 1.
Probom; PD000010; Homeobox; 1.
                     AE003589; AAF51473.1; -.
                                                                                                                                                                                                                                                                        100.00%
100.00%
1.12%
          AAB17948.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                  18
8.00
                                                                                                                                                                        169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                  P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                  Developmental
          052968;
                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                           2A5E_HUMAN
                                                                                                                                                                                                 DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPP2R5E
                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                       DOMAIN
                                                                                                                                                             DOMAIN
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          EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMPA_CHLPN STANDARD; PRT; 499 AA.
0928F8; 09JQJ2;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                          DD9CE11433F499CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                     467
8
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae (Chlamydophila pneumoniae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-667-170A-440 (1-2239) x 2A5E_HUMAN (1-467)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438 LysLysGluLysGluArgGluGlu 445
                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 AAGAAAGAAAAAGAGAGGGAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LAP) (Leucyl aminopeptidase). PEPA OR CPN0385 OR CP0370.
                                                                                                                                                                                                                                                                                                                                                                                           467 AA; 54699 MW;
                                                                                                                                                                                                                                                                         EMBL; 269029; CAA93153.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     17.7
8.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
                                                                                                                                                                                                                                                                                                                    Genew; HGNC:9313; PPP2R5E.
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002554; B56.
                                                                                                                                                                                                                                                                                                     AAB69752.1
                                                                                                                                                                                                                                                                                                                                                           Pfam, PF01603; B56; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=83558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CWL029
                                                                                                                                                                                                                                                                                                        EMBL; L76703;
                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                  MIM; 601647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-AR39
                                                                                                                                               FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
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                                                                                                                                                                                                                                                            xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro.
-!- COFACTOR: MANCANESE (BY SINILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M17.
                                                                                         Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314 (2000).

- FUNCTION: PRESUMABLY INVOLVED IN THE PROCESSING AND REGULAR TORNOVER OF INTRACELLULAR PROTEINS. CATALYZES THE REMOVAL OF UNSUBSTITUTED N-TERMINAL AMINO ACIDS FROM VARIOUS PEPTIDES (BY
                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-667-170A-440 (1-2239) x AMPA_CHLPN (1-499)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                 wucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Aminopeptidase; Manganese;
                                                                             MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000819; Peptidase_M17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00883; Peptidase_M17; 1.
Pfam; PF02789; Peptidase_M17_N; 1.
PRINTS; PR00481; LAMNOPPTDASE.
PROSITE; PS00631; CYTOSOL_AP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP002546; BAA98593.1; -. HSSP; P00727; 1BPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54509 MW;
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100.00%
1.12%
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pneumoniae AR39.";
                                                  SEQUENCE FROM N.A.
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499 AA;
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SEQUENCE
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                                                                                                                                                                                                                Mastroberardino L., Spindler B., Pfeiffer R., Skelly P.J., Loffing J., Shoemaker C.B., Verrey F.; Amino-acid transport by heterodimers of 4F2hc/CD98 and members of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99172172; PubMed=10072483;
Tsurudome M., Ito M., Takebayashi S., Okumura K., Nishio M.,
Rawano M., Kusaqawa S., Komada H., Ito Y.;
Primary structure of the light chain of fusion regulatory protein-
1/CD98/4F2 predicts a protein with multiple transmembrane domains that is almost identical to the amino acid transporter E16.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 light chain) (4F2 LC) (4F2LC) (CD98 light chain) (Integral membrane protein E16) (hLAT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prasad P.D., Wang H., Huang W., Kekuda R., Rajan D.P., Leibach F.H.,
Ganapathy V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human LAT1, a subunit of system L amino acid transporter: molecular cloning and transport function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A novel transiently expressed, integral membrane protein linked to cell activation. Molecular cloning via the rapid degradation signal
                                                                                                                                                                                                                                                                                                                                                                  'anagida O.', Segawa H., Miyamoto K., Takeda E., Goya T., Endou H.,
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY TRANSFORT OF LARGE NEUTRAL AMINO ACIDS. INVOLVED IN CELLULAR AMINO ACID UPPAKE.
-!- SUBUNIT: DISGULFIDE-LINKED HETERODIMER WITH THE AMINO ACID TRANSPORT PROTEIN SLC3AZ/4F2HZ.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN ADULT LUNG AND LIVE AND ILS ALSO EXPRESSED IN BRAIN, THYMUS, RETINA AND SOME OTHER
                                                                                                                                                                                                                                                                                                                                                                                                       Cloning and characterization of a human system L amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minato N., Iwal K., Takizawa C., Nakamura E.; "Human 4F2 light chain: amino acid transporter."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaugitsch H.W., Prieschl B.E., Kalthoff F., Huber N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 255:283-288(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 267-507 FROM N.A.
TISSUE-Peripheral blood lymphocytes;
MEDLINE-92283834; PubMed-1597461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=99160855; Pubmed=10049700;
                                                                                                                                                                                           MEDLINE=98421678; PubMed=9751058;
                                                                                                                                                                                                                                                                                         Nature 395:288-291(1998).
                                                                                 Homo sapiens (Human)
                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                        NCBI_TaxID=9606;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 light chain) (4F2 LC).
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N-LINKED (GLCNAC, ...) (POTENTIAL).
N-LINKED (GLCNAC, ...) (POTENTIAL).
A -> V (IN REF. 5).
AKS -> SKR (IN REF. 5).
T -> A (IN REF. 5).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       767F3C60B62C0F02 CRC64;
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T -> A (IN REF.
N -> K (IN REF.
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Matches:
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Interpro; IPR004760; L_AA_transport.
Interpro; IPR004841; Permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 TyrAlaGluLeuGlyThrThrIle 110
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                                                                                                                                                                                  Pfam; PF00324; aa_permeases; 1.
TIGRFAMS; TIGR00911; 2A0308; 1.
                                             154 T
230 N
55010 MW;
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8.00
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319
396
431
458
49
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                                                                                                                                                                                                                                                                                Nakamura E., Sato M., Yang H., Miyagawa F., Harasaki M., Tomita K., Matsuoka S., Noma A., Iwai K., Minato N.; Harasaki M. Tomita K., Minato N.; Liwai K., Minato N.; Larasporter and controls intracellular trafficking and membrane topology of 4F2 heterodimer.", J. Biol. Chem. 274:3009-3016(1999).
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8 N-LINKED (GLCNAC. . .) (POTENTIAL).
8 R -> M (IN REF. 2).
55902 MW; B3AE446E77374B0B CRC64;
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Mismatches:
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InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004641; Permease.
InterPro; IPR004841; Permease.
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MEDLINE=99115648; PubMed=9915839;
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TIGREAMS; TIGR00911; 2A0308; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLAND, AND UTERUS.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSPORT PROTEIN SLC3A2/4F2HC.
SUBCELLULALAR LOCATION: Integral membrane protein (Probable).
TISSUE SPECIFICITY: EXPRESSED HERATOMA BUT NOT IN NORMAL LIVER.
ALSO EXPRESSED IN PLACENTA, TESTIS, BRAIN, OVARY, SPLEES, MAMMARY
                                                                                                                                                                                                                                                                                                                  Sang J., Lim Y.P., Panzica M., Finch P., Thompson N.L.;
"TA1, a highly conserved oncofetal complementary DNA from rat
hepatoma, encodes an integral membrane protein associated with liver
development, carcinogenesis, and cell activation.";
Cancer Res. 55:1152-1159(1995)
-!- FUNCTION: SOLIUM-INDEPENDENT, HIGH-AFFINITY TRANSPORT OF LARGE
NEUTRAL AMINO ACIDS. INVOLVED IN CELLULAR AMINO ACID UPTAKE.
-!- SUBUNIT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACID
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                     063016; 090ML4;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last aguence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 LC) (4F2LC) (Integral SLC7A5 OR MPE16 OR TA1.
                                                                                                                                                                                                     Kanai Y., Segawa H., Myamoto K., Uchino H., Takeda E., Endou H.; "Expression cloning and characterization of a transporter for large neutral amino acids activated by the heavy chain of 4F2 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transport; Transmembrane.
            512 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004760; L_AA_transport.
InterPro; IPR004841; Permease.
                                                                                                                                                                                                                                           98).";
Biol. Chem. 273:23629-23632(1998).
                                                                                                                                                                                              MEDLINE=98395066; PubMed=9726963;
                                                                                                                                                                                                                                                                                             TISSUE=Hepatoma;
MEDLINE=95171385; PubMed=7532544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00324; aa_permeases; 1.
TIGRFAMS; TIGR00911; 2A0308; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB015432; BAA33035.1; -.
                                                                                                                                                                                                                                                                                SEQUENCE OF 272-512 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U00995; AAA74411.1;
            STANDARD;
                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
1167
1167
1194
229
2299
344
418
456
483
345
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                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279
324
338
436
463
50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSPORT PROTEIN SLC3A2/4F2HC.
--- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
--- TSSUE SPECIFICITY: MAINLY EXPRESSED IN KIDNEY AND INTESTINE.
--- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
--- PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEUTRAL AMINO ACIDS. HAS HIGHER AFFINITY FOR L-PHENYLALANINE THAT LATI. L-AARAINE IS TRANSPORTED AT PHYSTOLOGICAL CONCENTRATIONS. PLAYS A ROLE IN BASOLATERAL (RE)ABSORPTION OF NEUTRAL AMINO ACIDS. SUBUNIT: DISULFIDE-LINEED HEFERODIMER WITH THE AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "LAT2, a new basolateral 4F2hc/CD98-associated amino acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bassi M.T., Sperandeo M.P., Incerti B., Bulfone A., Pepe A., Surace E.M., Gattuso C., de Grandi A., Buoninconti A., Riboni M., Manzoni M., Andria G., Ballabio A., Borsani G., Sebastio G.; SLC7A8, a gene mapping within the lysinuric protein intolerance critical region, encodes a new member of the glycoprotein-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Large neutral amino acids transporter small subunit 2 (L-type amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid transporter family.";
Genomics 62:297-303(1999).
-i- FUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY TRANSPORT OF LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rossier G., Meier C., Bauch C., Summa V., Sordat B., Verrey F.,
B487CE0B58D73A02 CRC64;
                                                                                             512
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                                                                                                                                                             Conservative:
                                                                                                                                                                                               Mismatches:
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                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                       (1-512)
                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of kidney and intestine.";
J. Biol. Chem. 274:34948-34954(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y19022; CAB69072.1; -.
MGD; MGI:1355323; S1c7a8.
InterPro; IPR002293; AA/rel_prmeasel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=20044753; PubMed=10574970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20079165; PubMed=10610726;
                                                                                                                                                                                                                                                                                                                       US-09-667-170A-440 (1-2239) x LAT1_RAT
                                                                                                                                                                                                                                                                                                                                                                                       517 TATGCTGAATTGGGAACAACTATA 540
                                                                                                                                                                                                                                                                                                                                                                                                                            104 TyrAlaGluLeuGlyThrThr11e 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF171668; AAF20380.1; -.
   512 AA; 55903 MW;
                                                                                                                                                          100.00%
100.00%
1.09%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transporter 2).
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                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLC7A8 OR LAT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY.
                                                                                                                                                                Percent Similarity:
                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAT2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuhn L.C.;
      SEQUENCE
                                                                                                                                                                                                                             Query Match:
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No.:
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DR InterPro; IPR004766; L_AA_transport.

DR Pfam; PF00324; aa_permeasse.

P Fam; PF00324; aa_permeasses; 1.

DR TGRPAMS; TIGR00911; 2A0308; 1.

KW Transport; Amino-acid transport; Transmembrane.

FT TRANSMEM 12 132 POTENTIAL.

FT TRANSMEM 154 174 POTENTIAL.

FT TRANSMEM 154 174 POTENTIAL.

FT TRANSMEM 267 287 POTENTIAL.

FT TRANSMEM 309 329 POTENTIAL.

FT TRANSMEM 309 329 POTENTIAL.

FT TRANSMEM 387 407 POTENTIAL.

FT TRANSMEM 421 441 POTENTI
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US-09-667-170a-440 (1-2239) x LAT2_MOUSE (1-531)
Qy 1126 TCAAATGCAGTGGCAGTGACCTTT 1149

Search completed: April 16, 2003, 16:36:44 Job time: 33.5 secs

Perfect score:

Run on:

Sequence:

Scoring table:

Minimum DB Maximum DB

Database :

Word size:

Searched:

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055384 synechocyst 05482 mus musculu 05583 arabidopsis P04060 arabidopsis P04060 arabidopsis 09tip 4 taenia cras 09tip 4 musculu 058784 arabidopsis 09587 trypanosoma 098784 arabidopsis 09615 homo sapien 024300 drosophila 09v9d6 drosophila 09eb06 sesbania mo 099891 mus musculu
                                                                                                                                           0915K5 pseudomonas
0977t5 uncultured
093019 rhizobium m
095596 arabidopsis
005684 saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  064460 citrus jamb
080421 citrus iyo.
09say9 citrus iyo.
09zwh6 poncirus tr
08s988 microcitrus
                                         rattus norv
                                                    rattus norv
                                                                         Q9jmh8 mus musculu
                                                                                   O9xmpl ceratitis c
O57439 xenopus lae
                                                                                                           013020 xenopus lae
                                                                                                                                     mus musculu
                                                                                                                                                                                                                                                                                                                                                                                               09a101 streptococc
08xvm8 ralstonia s
08zwh2 pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                               Oguzg6 pyrococcus
Ogtsy3 methanosarc
O94824 tetrahymena
                                                                                                                       Q8rg74 fusobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                         pyrobaculum
    29plx0 homo sapien
                                                              Q9ns82 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human cystine/glutamate exchanger: cDNA cloning and upregulation by oxidative stress in glioma cells."; submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB040875; BA840574.1; InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004841; Permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim J.Y., Chairoungdua A., Cha S.H., Segawa H., Matsuo H., Kim D.K., Endou H., Kanai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   99zb60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                  Q9R0S5
Q9Q266
Q9NS82
Q9JMH8
Q9JMH8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel, 17, Created)
                                                                                                                                                                                                               Q9D4S2
O65683
P94060
                                                                                                                                                                                                                                                                                                                                                                                                                    Q8ZWH2
Q9UZG6
Q8TSY3
                                                                                                        O13020
Q8RG74
                                                                                                                                                                                                                                                                                                                                                          Q8REU5
Q9EB06
Q99K91
                                                                                                                                            0915K5
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08XVM8
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                                                                                                                                 Q8VED7
                                                                                                                                                                   Q930L9
                                                                                                                                                                               090596
                                                                                                                                                                                                     055384
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Q9V9D6
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                                                                                                                                                                                         005684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cystine/glutamate exchanger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
 Q9BYH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09BYH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
Q9BYH2
MODEL-frame+_n2p.model -DEV=xlh
-Q-Cgn2_1/USPTO_spool/US09667170/runat_04042003_091001_21199/app_query.fasta_1.2375
-DB-SPTREMBL_21 -QFWT-fastan -SUFFX-olin2p.rspt -MINRATCH-0.1 -LOOPCL=0
-LOOPEXT-0 -UNITS_bits -STAR*-1 -END=-1 -MATRIX-olingo -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE-quality -THR_MIN=1 -ALIGN=15 -MODE-LOCAL
-USFR-USP09667170_eCGN_1 _1 122_erunat_042003_091001_21199 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEY_TIMEOUT=120
-WARN_TIMEOUT=0 -THREADS=1 -XGAPDEXT=60 -KGAPOP=6 -FGAPDEXT=7
                                                                                     (without alignments)
9561.440 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                            Description
                                                                      April 16, 2003, 16:27:06 ; Search time 96.5 Seconds
   GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                               OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        671580 seqs, 206047115 residues
                                                                                                                                                                              5 60.0 , Xgapext 60.0
5 60.0 , Ygapext 60.0
6.0 , Fgapext 7.0
6.0 , Delext 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                 Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_vertebrate:*
sp_unclassified:*
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sp_invertebrate:*
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Score Match Length DB ID
                                                                                                                       US-09-667-170A-440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_organelle:*
                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 20000000000
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sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_archeap:*
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446

Result . 0

DR SQ	TIGRI SEQUI	FAMS; TIGR0091 ENCE 494 AA;	1; 2A0308; 1. 54423 MW; BE	C57A7EA4DDB0B1	CRC64;	
Aligni Pred. Score Percel Best Query DB:	ment No.: nt S Loca Mat	Scores: : imilarity: l Similarity: ch:	0 446.00 100.00% 100.00% 60.93%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	494 446 0 0 0	
0S-09	-667	-170A-440 (1-2	(239) x Q9BYH2 (1-494)		
QY	334	GAGAAAGTGCAGC	CTGAAGAGGAAAGTCA 	ACTTTACTGAGGGGAGT	TCTCCATTATCATTGGC	393 55
ογ		TTGG	AATCTTCATC	CTCCTAAGGGCGT	FCCAGAACACGGGCAG	
g d	Ŋ	Thrileileg				S
Οy	454	SGGCATGI	CATCI	GTGGGGTCCTGT	CACTATITES	513
qq	16	ValGlyMetS	erLeuThrIleTrpThrValC	ysGlyValLeus	erLeuPheGlyAlaLe	95
Oy Db	514	TCTTATGCT	GAATTGGGAACAACTATAAAC 	SAAATCTGGAGGTC	ATTACACATATATTTTG	573 115
ô		GAAGTCTT	CAGCI	TCTGGGTG	CATAATACG	'n
- qa	-	GluValPhe			GluLeuLeuIleIleArg	
δy	634	: :	SCTGTGATATCCCTGG	SCATTIGGACGCTACA	CTGGAACCATTTT	693
qq	136	ProAlaAlaThrAlaValI	AlaValIleSerLeuA	IleSerLeuAlaPheGlyArgTyrIle		155
Oy Dp	694	ATTCAATGTC	SAAATCCCTGAACTTGCGA 	CGATCAAGCTCATTACAG(CAGCTGTGGGCATAACTGTA	753
οy	754	GTGATGGTC		GCCCGGA	rccagattttcttaac	813
qq	176	ValMetVal	[SerTrpSerAlaArgi	leglnilePheLeuThr	195
Οy	H		TTTGCAAGCTCACAGCAATTCTGATAATTATAGT	ATTATAGTCCCTGGAG	CCCTGGAGTTATGCAGCTAATTAAA	7
q	196		rhrAlaIleLeuIleI	[leIleValProGlyVa	alMetGlnLeuIleLys	215
oy t	874	0 - 0	GTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGAAGAGT"	TTTCAGGAAGAGATT	TCAAGTATTACGCGGTTG	933
3 6	4 10	י כ	rankhengsaspatat Pattatgaatgtatg	SCATATGCTGGCTGGT	TTTACCTCAACTTTGT	, ס
g 2	m	ProLeuA		AlaTyrAlaGlyTrpP		Ŋ
03	994	ACTGAAGAAGTAGA	AAACC	ACCATTCCCCTTGCAA	FA -	1053
qq	256	TH	uAsnP	roGluLysThrIleProLeuAlaIl	ecyslleSerMetAl	275
Qy	1054	ATTGTCACCATT	GGCTATGTGCTGACAAATG	AATGTGGCCTACTTTACGACC	ATTAATGCT	1113
qq	276	IleValThrIle	lyTyrValLe	alAla	IleAsnAlaG	295
δō i	<i>→</i> 0	GAGCTGCTGCT	TTCAAATGCAGTGGCAGTC	STGACCTTTTCTGAGCGGC	GGCTACTGGGAAATTTC	
2	<u>, </u>	етпаппаппта	SELASIBATAVAL	TIII FIIESEIGTUR	יבחדים	313
Qy	1174 316	TCATTAGCAGTT	CGATCTTTGTT 	GCCCTCTCCTGCTTTGGCT 	CCATGAACGGTGGTGTG 	1233 335

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1354 ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTGAATTTCCTCAGTTTTGCC 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1474 GATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGC 1533
1234 TTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
                                                                                                                   1294 TCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTG 1353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1534 CTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1593
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                                                                                                                                                MEDLINE=21082210; PubMed=11213471;
Sato H., Tamba M., Kuriyama-Matsumura K., Okuno S., Bannai S.;
"Molecular cloning and expression of human xCT, the light chain of amino acid transport system xc.";
amino acid transport system xc.";
amino acid transport system xc.";
amino acid transport system inc.";
amino acid transport system xc.";
amino acid transport system xc.";
Intication: Redox Signal. 2:665-671(2000).

EMBL; AB042201; BAA94999.1;
InterPro; IPR002293; AA/rel_prmeasel.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OMAR-2002 (TrEMBLrel. 20, Last annotation update)
Cystine/glutamate transporter (Fragment).
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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SEQUENCE
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RESULT 6
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56 ThrileileGlyAlaGlyIlePheileSerProLysGlyValLeuGlnAsnThrGlySer 75
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Y-LAVIa (Solute carrier family 7 (Cationic amino acid transporter, y+
system), member 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NIH/SWISS; TISSUE=HEART;
MEDLINE=99094891; PubMed=9878049;
Pfeiffer R., Rossier G., Spindler B., Meier C., Kuhn L., Verrey F.;
"Amino acid transport of Y+L-type by heterodimers of 4F2hc/CD98 and members of the 91ycoprotein-associated amino acid transporter family.";
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                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10909;
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01-MAR-2002 (TEEMBLEL. 20, Last annotation update)
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Mismatches:
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EMBL, AJ130943; CAA10555.1;
EMBL, AJ13043; CAA10555.1;
InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004841; Permease.
                                                                                                                                                                                            PRT;
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MEDLINE=99094891; PubMed=9878049;
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EMBO J. 18:49-57(1999).
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Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kanai Y., Fukasawa Y., Segawa H., Endou H.;
"Characterization of a system y+L amino acid transporter.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020520; BAAG7325.1;
InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004841; Permease.
                               Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ012754; CAA10170.1;
EMBL; BC014709; AAH14709.1;
                                                                                                                                                                                                        9F30FB1B88126F6C CRC64;
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SEQUENCE 512 AA; 55641 MW; 708905B2ACB0A824 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                              517 TATGCTGAATTGGGAACAACTATAAAGAAATCTGGA 552
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Matches:
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                                                                                                     MGD; MGI:1337120; S1c7a7.
InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004841; Permease.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-WAR-2002 (TrEMBLrel. 20, Last anno
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                                                                                                                                                        Pfam; PF00324; aa_permeases; 1.
                                                                                                                                                                                                    SEQUENCE 510 AA; 55677 MW;
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Best Local Similarity: 100.00%
Query Match: 1.64%
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[2]
SEQUENCE FROM N.A.
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                    Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leclerc D., Wu Q., Ellis J.R., Goodyer P., Rozen R.; ^{\circ} Is the slc7al0 gene on chromosome 19 a candidate locus for
                                                                                             STRAIN-SPRAGUE-DAWLEY;
STRAIN-SPRAGUE-DAWLEY;
MDA AM.L., Yao S.Y.M., Cheeseman C.I., Young J.D.;
"CDMA encoding rat joinual amino acid transporter y+LATI.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF200684; AAF07216.1;
InterPro; IPR002293; AAA/rel_prmeasel.
InterPro; IPR004841; Permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borsani G., Nunes V., Palacin M.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB037670; BAB03213.1; -.
EMBL; AF340165; AAK93960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ASC-type amino acid transporter 1 (ASC1 protein).
                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                           517 TATGCTGAATTGGGAACAACTATAAAGAAATCTGGA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                              523 AA.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genet. Metab. 73:333-339(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=21400982; Pubmed=11509015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with high affinity.";
Neurosci. Lett. 287:231-235(2000).
                                                                                                                                                                                         Pfam; PF00324; aa_permeases; 1.
SEQUENCE 512 AA; 55684 MW;
     Amino acid transporter y+LAT1.
Rattus norvegicus (Rat).
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                                                                                   SEQUENCE FROM N.A.
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SPECIES-Mouse; Med-10734121; Chairoungdua A., Kim D.K., Fukasawa 20200467; PubMed-10734121; Fukasawa Y., Segawa H., Kim J.Y., Chairoungdua A., Kim D.K., Matsuo H., Cha S.H., Endou H., Kanai Y.; "Identification and characterization of a Na+-independent neutral amino acid transporter that associates with the 4F2 heavy chain and exhibits substrate selectivity for small neutral d- and l- amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning and characterization of a D-serine transporter from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OC5A80BF922DB54D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-Rat; STRAIN-SPRAGUE DAWLEY; TISSUE-FOREBRAIN; Alberati-Giani D., Kew J.N.;
                                                                                                                                                                                                                                                                                     56797 MW; 24BA0B36521AC2D4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
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Matches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-667-170A-440 (1-2239) x Q9NS82 (1-523)
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Interpro; IPR004841; Permease.
                                                                                                                                                                                                       EMBL; A1277731; CAC81900.1; -.
INTERPRO; IPR002293; AA/rel_prmeasel.
Interpro; IPR004841; Permease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 275:9690-9698(2000).
                                                          EMBL; AF340158; AAK93960.1; JOINED. EMBL; AF340159; AAK93960.1; JOINED.
                                                                                                                                                                JOINED.
                                                                                                                       EMBL; AF340161; AAK93960.1; JOINED.
                   AAK93960.1; JOINED.
AAK93960.1; JOINED.
                                                                                                   EMBL; AF340160; AAK93960.1; JOINED.
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AF340155; AAK93960.1; JOINED
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SEQUENCE 530 AA; 57548 MW;
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                                                                                                                                                                                                                                                                    Pfam; PF00324; aa_permeases; croffence 523 AA; 56797 MW
                                                                                                                                            EMBL; AF340162; AAK93960.1;
                                                                                                                                                                EMBL; AF340163; AAK93960.1;
EMBL; AF340164; AAK93960.1;
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Query Match:
                                           AF340157;
                          AF340156;
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Tephritoidea; Tephritidae; Ceratitis.
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MEDLINE-99047611; PubMed-9829974;
TOTTENTS D., Estevez R., Pineda M., Fernandez E., Lloberas J.,
Shi Y.B., Zorzano A., Palacin M.;
"Identification and characterization of a membrane protein (y+L amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
L amino acid transporter-1 LAT-1.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDIINE=20225575; PubMed=10762421;
Spanos L., Koutroumbas G., Kotsyfakis M., Louis C.;
"The complete sequence of the mitochondrial genome of the Medfly, Ceratitis capitata.",
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NADH dehydrogenase (ubiquinone) chain 2 (EC 1.6.5.3).
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      Conservative:
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Mismatches:
                  Mismatches:
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                                                             US-09-667-170A-440 (1-2239) x Q9JMH8 (1-530)
                                                                                     409 GGAATCTTCATCTCCTAAGGGCGTGCTC 438
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NCBI_TaxID=8355;
Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                     Mitochondrion
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                           Query Match:
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Mastroberardino L., Spindler B., Pfeiffer R., Skelly P.J., Loffing J., Shoemaker C.B., Verrey F., Amino acid transport by heterodimers of 4F2hc/CD98 and members of a
acid transporter-1) that associates with 4F2hc to encode the amino acid transport activity y+L. A candidate gene for lysinuric protein intolerance.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Bukaryota, Metrazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spindler B., Mastroberardino L., Custer M., Verrey F., "Characterization of early aldosterone induced RNAs in A6 kidney epithelia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G -> A (IN REF. 0).
A -> R (IN REF. 0).
F -> L (IN REF. 0).
A -> D (IN REF. 0).
A -> D (IN REF. 0).
A -> D (IN REF. 0).
                                                                                                                                                    EA0E9782B3313B82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AuG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Amino acid transporter chain (AmAt-L-lc) ASUR4.
                                                                                                                                                                                                                             Conservative:
Mismatches:
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                                                                       InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004760; L_AA_transport.
InterPro; IPR004841; Permease.
                                             Chem. 273:32437-32445(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mature 395:288-291(1998).

EMBL: Y12716: CAA73254.1; -.
InterPro: IPR002293: AA/rel_prmeasel.
InterPro; IPR004841; Permease.
                                                                                                                                                                                                                                                                                                                               610 TGGGTGGAACTCCTCATAATACGCCCT 636
                                                                                                                                                                                                                                                                                                                                                134 TrpValGluLeuLeuIleIleArgPro 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-AUG-1998 (TrEMBLrel. 07, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97324256; PubMed=9178633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pflugers Arch. 434:323-331(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98421678; PubMed=9751058;
                                                                                                                 Pfam; PF00324; aa_permeases; 1
TIGRFAMS; TIGR00911; 2A0308; 1.
SEQUENCE 507 AA; 55595 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00324; aa_permeases; 1
TIGRFAMS; TIGR00911; 2A0308; 1
CONFLICT 42 42 6
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                                                                                                                                                                                                                          Percent Similarity:
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                                                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                             Pred. No.:
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 RT RT RT DR DR DR DR DR DR DR SQ
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Alignment Scores:
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                         Score:
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FMBI. AEQUISSE; ALGH94639.1; Complete Proteome.

SEQUENCE 57 AA, 6601 MW; 609693E522C2F9AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mūs musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO19134; AAH19134.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 AA; 7700 MW; D2D9A9CC193308C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 7.7 kDa protein (Fragment).
                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein FN0443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
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                                                                                                                                               57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                 Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                 Indels:
                            Gaps:
                                                   US-09-667-170A-440 (1-2239) x 013020 (1-507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-667-170A-440 (1-2239) x Q8RG74 (1-57)
                                                                           610 TGGGTGGAACTCCTCATAATACGCCCT 636
                                                                                        134 TrpValGluLeuLeullelleArgPro 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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      Best Local Similarity: 100.00%
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                 . 238
                                                                                                                                                   PRELIMINARY;
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Best Local Similarity:
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                                                                                                                                                                                                                                                          NCBI_TaxID=76856;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                               Q8RG74;
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                     Query Match:
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                                                                                                                                       Q8RG74
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Dham X.O.T., L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Golttry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 AA; 8377 MW; 25FD055DA4661504 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Small membrane protein.
                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
coat protein B of bacteriophage Pf1.
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Mismatches:
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                                                                                                     Gaps:
                                                                                                                                         US-09-667-170A-440 (1-2239) x Q8VED7 (1-65)
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                                                                                                                                                                                                      31 PhePheLeuSerPhePheLeu 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                opportunistic pathogen.";
Nature 406:559-964(2000).
EMBL, FAEO44577, AAG04112.1; -
HSSP; P03621; 1PFI.
                                                                                                                                                                                 90 TITITICITICITICITITICCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
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                                            Percent Similarity:
Best Local Similarity:
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          Pred. No.:
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RA Beja O., Koonin E.V., Aravind L., Taylor L.T., Seitz H., Stein J.L.,
RA Bensen D.C., Feldman R.A., Swanson R.V., DeLong E.F.;
RT "Comparative genomic analysis of coexisting archaeal genetic variants
RT in an Antarctic marine microbial assemblage.";
R. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
B. Shubitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
SQ SEQUENCE 89 AA: 9325 MW; B4E02F76DBE2F393 CRC64;
Alignment Scores: 95.3 Length: 89
Rocent Similarity: 100.00% Matches: 0
Best Local Similarity: 100.00% Mismatches: 0
Best Local Similarity: 1.09% Indels: 0
Best Local Similarity: 1.09% Gaps: 0
Conservative: 0
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Best Local Similarity: 1.09% Gaps: 0
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Search completed: April 16, 2003, 16:40:12 Job time: 104.5 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                         OM nucleic - protein search, using frame_plus_n2p model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Maximum DB seq length: 200000000
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COmmand line parameters:

-WODEL-frame+_n2p.model -DEV-x1h
-O-YG902_1/05P00_spool/US09667170/runat_04042003_090918_20307/app_query.fasta_1.2375
-O-YG902_1/USPTO_spool/US09667170/runat_04042003_090918_20307/app_query.fasta_1.2375
-UB-PIR_73 -QFWT=fastan -SUFFIX=-DEP.FIX -NIAMATGH=0.1 -LOOPCE_0 -LOOPEXT=0.
-UNITS-bits -START=1 -END-1 -MATRIX=bloosum62 -TRANS-buman40.cdi -LIST=45
-UOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORM=ext -HERASIZE=500 -MINLENO -MAXLEND-2000000000
-USER-0509667170_eCGN_1 1_57_erunat_04042003_090918_20307 -NCPU=6 -LOPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEY_TIMEOUT=120
-WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

Database :

pir1:* pir2:* pir3:* pir4:* PIR_73:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	LATI protein - hum hypothetical prote amino acid permeas hypothetical prote amino acid transpo cationic amino aci methionine transpo
SUMMARIES	JG1165 T214165 T21419 T228118 T15226 T12821 T15824 T16854 T24837 B69855 B89921 A11995 B69172
08	000000000000000
% Query Match Length DB	5 6 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
å Query Match	25.74 25.74 25.74 25.77 25.77 10.23
Score	1210.5 975 910 910 715 665.5 622.5 622.5 564 521.5 479.5 463.5
Result No.	201 100 110 111 113

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D87396 S48932 TAEL155 T34694 AH1513 E691156 B860105 E651156 B860105 E71651 C69451 E71651 F716	00000
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11111022222222222222222222222222222222	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

JG0165

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C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 17-Nov-2000
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 17-Nov-2000
C;Accession: JGOL65; A42783
R;D.Prasad, P.; Wang, H.; Huang, W.; Kekuda, R.; P.Rajan, D.; H.Leibach, F.; Ganapath Biochem. Biophys. Res. Commun. 255, 283-288, 1999
A;Tille: Human LAT1, a subunit of system L amino acid transporter: Molecular cloning A;Reference number: JGOL65; MUID:99160855; PMID:10049700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Cross-references: GB-AF104032; NID:94426639; PIDN:AAD20464.1; PID:94426640
F/Gaugitsch, H.W., Prieschl, E.E.; Kalthoff, F.; Huber, N.E.; Baumruker, T.
J. Biol. Chem. 267, 11267-11273, 1995
A/Title: A novel transiently expressed, integral membrane protein linked to cell acti
A/Reference number: A42783; MUID:92283834; PMID:1597461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Experimental source: peripheral blood lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:104749, NCBIP:104750)
C:Superfamily: arginine permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 267-507 <GAU>
A;Cross references: GB:M80244; NID:g181907; PIDN:AAA35780.1; PID:g181908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-507 <DAP>
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A; Status: preliminary
LAT1 protein - human
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507 232 95 164

Conservative: Mismatches: Matches: Length:

6.65e-100

1210.50 66.19%

Best Local Similarity:

Query Match:

Percent Similarity:

US-09-667-170A-440 (1-2239) x JG0165 (1-507)

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1081 AATGIGGCCTACTITACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1141 GIGACCTTITCIGAGCGGCIACTGGGAAATTICICATIAGCAGTICCGAICTITGIIGCC 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1201 CTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCCAGGTTATTCTAIGTT 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 PheGluGlyThrLysLeuAspValGlyAsnIleValLeuAlaLeuTyrSerGlyLeuPhe 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaThrArgValGlnAspAlaPheAlaAlaAlaLysLeuLeuAlaLeuAlaLeuIleIle 212
                                                                                                                                                                                                                                                                                                                              547 ICIGGAGGICATIACACATATATITIGGAAGICTITGGICCATIACCAGCTTTIGIACGA 606
                                                                                                                                                                                                                                                                                                                                                                                                                   667 GGACGCIACATTCTGGAACCATTTTTTTTTCAATGTGAAATCCCTGAACTTGCGATCAAG 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 AlaThrTyrLeuLeuLysProLeuPheProThrCysProValFroGluGluAlaAlaLys 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 LeuValAlaCysLeuCysValLeuLeuLeuThrAlaValAsnCysTyrSerValLysAla 192
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                                                                                                                                                                                                                                                                 GGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAA 546
                                                                                                                                                                                                                                                                               CTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGG 786
                                                                                                                              367 CTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCTCT 426
                                                                                                                                                                                              427 AAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGGACCATCTGGACGGTGTGT 486
247 CCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACGCCTTT 306
                                                                 107 TCAGGAAGAGGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTA 366
                                                                                      53 LeuAsnGlyValAlaileileValGlyThrileileGlySerGlyIlePheValThPro 72
                                                                                                                                                                                                                 607 GICTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGCATTT
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A;Cross-references: EMBL:268216; PIDN:CAA92459.1; GSPDB:GN00022; CESP:F27C8.1
A;Experimental source: clone F27C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
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1321 CCTCTACCAGCTGTTATTGTTTTTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGAC 1380
                                                                            1381 CTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTATTGGGCTGGCAGTT 1440
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                                                                                                    453 LysThrProValGluCysGlyIleGlyPheThrIleIleLeuSerGlyLeuProValTyr 472
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A;Introns: 60/1; 162/1; 204/1; 255/2; 385/3; 443/1; 474/1
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A; Accession: T21445
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-493 <WIL>
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Best Local Similarity:
Query Match:
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R; Lloyd, C.
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997 GAAGAAGTAGAAAACCCTGAAAAACCATTCCCCTTGCAATATGTATACCATGGCCATT 1056
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88 LeuGlyThrLeuIleLysLysSerGlyGlyAspTyrAlaTyrIleWetGluAlaPheGly 107
                                 586 CCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACT 645
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|108 ProphevalAlaPheIleArgLeuTrpIleGluAlaIleValValArgProCysThrVal 127
                                                                                                  646 GCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAACCATTTTTTATTCAATGTGAA 705
                                                                                                                                                                  706 ATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTA 765
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                                                                                                                         128 ThrIleValAlaLeuThrPheAlaIleTyrGlyLeuArgPrOPhePheProAspCysAla 147
                                                                                                                                                                                             766 AATAGCATGAGTGTGAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTC 825
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248 GluGluLeuGlnAsnProLysArgAsnLeuProLeuAlalleAlalleSerlleThrSer 267
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A;Map position: X
A;Introns: 20/3; 60/1; 123/2; 162/1; 204/1; 255/2; 296/3; 329/1; 401/2; 433/3; 544/1
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A.Reference number: 221175
A.Accession: T32479
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-563 <CHI>
A.Residues: 1-563 <CHI>
A.Cross-references: EMBL:AF026214; PIDN:AAB71312.1; GSPDB:GN00028; CESP:F52H2.2
A.Experimental source: strain Bristol N2; clone F52H2
                                                                                                                                                                                                                   C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Jun-2000
C; Accession: T32479
R; Chissoe, S.; Hawkins, J.
Submitted to the EMBL Data Library, September 1997
1654 TGGTTTAGAATAATGTCAGAGAAAATAACCAGAACATTACAAATAATACTGGAAGTTGTA 1713
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| 468 TrpPheAsnGluPhelleAspSerSerThrValPheIleGlnLysLeuPheMetValVal 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586 CCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACT 645
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106
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                                                                                                                                                                                                  hypothetical protein F52H2.2 - Caenorhabditis elegans
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Matches:
Conservative:
Mismatches:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1504 TTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTATTCG 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------TITIGCTGTCTCCAGGTTATTCTATGTTGCGTCT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1267 CGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGCTGTTATTGTTTTGCACCCTTTGACAATGATA---ATGCTCTTCTCTGGAGACCTC 1383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1177 TTAGCAGTICCGAICTITGITGCCCTCTCCTGCTITGGCICCAIGAACGGTGGIGTG--- 1233
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448 TyrSerLeulleAsnTyrIleGlnValSerTyrTrplleAlalleGlyGlyAlalleLeu 467
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                                                                                                                                                                                                                                                                                                                                                         1057 GTCACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAG 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                1117 CIGCIGCITICAAATGCAGIGGCAGIGACCITITICIGAGCGGCIACIGGGAAAITICICA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 GlyAsnArgGlnLeuProPhePheGluAsnPhePheValGluIleIlePheLeuSerAla 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 LeuGluLysSerMetValValPhePhePheTyrSerGluThrLeuPheTyrCysGlyAla 407
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408 argGluGlyGlnMetProAsnValLeuThrMetValAsnLysThrThrLysThrProIle 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 ThrArgLeuCysGlySerArgAspValArgGlnAlaAlaIleAlaGluValAlaGluPro 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 GlnAsnProLysIlePheGlyAsnArgGlnLeuProAsnLeuThrSerGlnLysIlePhe 367
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                                                                                                                                                                              937 CTGGCTTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTACCTCAACTTTGTTACT 996
                                                                                                                                                                                                     826 ACAGCAATICTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAG 885
                                208 AlaPheAspSerPheGluAsnIlePheGluAsnThrAlaLySAspLeuGluThrAlaSer 227
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A;Molecule type: DNA
A;Residues: 1-464 <FAV>
A;Cross-references: EMBL:U50308; PIDN:AAC48006.1; GSPDB:GN00023; CESP:F07C3.7
A;Experimental source: strain Bristol N2; clone F07C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 ThrPhelleAsnCysTrpAspValArgMetAlaThrArgThrAsnAspPhePheThr1le 170
                                                                                     C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000
C;Accession: T28818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    757 ATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTT 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 GGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCT 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            817 IGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGT
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185
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                                                                                                                                                   R.Fravello, A.; Gattung, S. submitted to the EMBL Data Library, March 1996 A.Description: The sequence of C. elegans cosmid F07C3. A.R.Reference number: Z20528 A.R.Reference number: Z20528
                                                                         hypothetical protein F07C3.7 - Caenorhabditis elegans
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548 IlePheThrGlnLysLeuPheMetValval 557
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A; Introns: 91/3; 240/2; 272/3; 299/2
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A;Accession: T15226
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-566 <GOE>
A;Cross-references: EMBL:AF003144; NID:g2088754; PID:g2088757; PIDN:AAB54195.1; GSPDB:GN
                                                                                                          991 GTTACTGAAGAAGTAGAAAACCCTGAAAAACCATTCCCCTTGCAATATGTATATCCATG 1050
                                                                                                                                                                                   1051 GCCATTGTCACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCT 1110
                                                                                                                                                                                                                                                            1111 GAGGAGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAAT 1170
                                                                                                                                                                                                                                                                                                                                     1171 TICTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGT 1230
                                     931 TIGCCACTGGCTITTTATTATGGAATGTATGCATATGCTGGCTGGTTTTACCTCAACTTT 990
                                                                      211 IlealaMetalaPheTyrSerGlyValPheSerPheSerGlyPheSerTyrLeuAsnPhe 230
                                                                                                                                  1231 GTGTTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATC 1290
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191 HislieAspAsnLeuValMetProAspValAlaGluGlySerGlnThrLysLeuSerAla 210
                                                                                                                                                                                                           1411 GCCAGGTGGCTTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGC 1470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1522 TCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTAT---TCGGACCCATTAGTACA 1578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::|||||| :::||||::: ||||||:::|||| |||| 314 PheAlaMetIleSerIleArgGlnLeuThrProlleProSerLeuIlePheLeuGlyGly 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 ThrserilevalMetLeuPheileGlyAsnValPheGlnLeulleAsnTyrLeuSerPhe 353
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C'Species: Caenorhabditis elegans
C'Accession: T15226
R'Goela, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 LysTyrArgProGlyPheIleGlnSerValTrpIleGlyPheThrHisPheIleGlnLys 453
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A;Description: The sequence of C. elegans cosmid C55C2.
A;Reference number: 218311
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334 GAGAAAGIGCAGCIG-----AAGAGGAAAGTCACTTTACIGAGGGAGICTCCAIT 384
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                                                                                                                                                                                                                                                                                                25 GluAsnThrGlnIleMetAspGluSerHisLysMetGlyPheLeuGlyAlaThrSerTyr 44
                                                                                                                                                                                                                                                                                                                                                       625 ATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAA 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 GlyLeuLysGlnTyrTyrGluIleAspAspAlaLeuValProThrCysGlnLysLeuPhe 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     733 ACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGC---TGGAGC 789
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                                                                                                                                                                                                                                                                                                                                                                                                                    165 AlaTyrSerLeuLeupheLeuValThrTrpMetAsnPhePheGluLeuSerLysPheAla 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    790 GCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATAATTATAGTC 849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 ThrGlyPheTyrPheTyrPheValLysGlyTrpHisGlyTyrLeuGluAsnProMetGln 224
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                                                 A;Map position: 1
A;Introns: 85/1; 148/3; 170/1; 214/1; 303/3; 370/3; 426/2; 481/1; 550/2
                                                                                                                           566
159
107
205
14
A: Experimental source: strain Bristol N2; clone C55C2
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54.85%
32.78%
17.35%
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                 C;Genetics:
A;Gene: CESP:C55C2.5
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A; Molecule type: DNA
A; Residues: 1-662 <MAG>
A; Cross-references: EMBL:AF040647; PIDN:AAB94996.1; GSPDB:GN00020; CESP:F54D12.3
A; Experimental source: strain Bristol N2; clone F54D12
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                            1267 CGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTA 1326
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                                                                                                                                                                                                                                      365 valAlaValLeuAlaGlnSerValLeuAlaLeuValIleSerTyrIleGlyAspLeuAsp 384
                                                                              345 ArgGlnGlyHisLeuProAlaCysPheSerCysValAsnThrGluThrGluSerProArg 364
A:Map position: 2
A:Introns: 31/1; 88/2; 191/1; 235/1; 304/1; 396/2; 443/3; 510/3; 584/3
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R;Maggi, L.; Goela, D.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F54D12.
A;Reference number: 221228
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Conservative:
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Best Local Similarity:
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US-09-667-170A-440 (1-2239) x T32821 (1-662)

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871 AAAGGICAAACGCAGAACTITAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGG 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 ThrLysasnalaLysasnProaspPheProLysasnIlePheargargProLeuAlaSer 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGATATCCCTG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 SerPheMetTrpValSerThrCysLeuSerTyrProAlaValLeuAlaIleGlnAlaIle 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 SerPheGlyGluTyrIleValThrGluLySLySThrLySIleLeuLySLySLySLySPhe 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 SerGlnPhePheHisThrLysAsnAlaThrLysSerHisArgThrHisPheSerVallle 186
                                                                                                                                                                                                                                                                                                                                                                                                                          127 PhellellePhePheArgLysPheMetSerPheArgLeuLysLysLeuArgPheLeuLys 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 SerpheThrProllePheLeuThrPheIleThrGlnAsnValThrLysIleAlaIleIle 166
                                                                                                                                                                                                                                                                                                                                                           107 GluLysLysCysValGluLeuLysPheThrLeuAspPheThrGlnAsnSerGluLysAsn 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                             577 GTCTTTGGTCCATTA----- 591
                                                                                                                                457 GGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCT 516
                                                                                                                                                                                             517 IATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATT----- 570
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337 AAAGTGCAGCTGAAGAGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGCACC 396
                                                                397 ATCATTGGAGCAGGAATCTTCATCTCTCTAAGGGCGTGCTCCAGAACACGGGCAGCGTG 456
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991 GTTACTGAAGAAGTAGAAAACCCTGAAAAACCATTCCCCTTGCAATATGTATATCCATG 1050
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                                                                                                                                                                                                                                1111 GAGGAGCTGCTTTCAAATGCAGTGGCAGTG-------ACCTTTTCT 1152
                                                                                                                                                                                                                                                                                                            GAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTT 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1273 GGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCT 1332
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|||||||
407 AlaileSerAlaThrValPheIleLeuMetAsnValSerTyrPheSerValLeuSerVal 426
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| 427 GluAspPheLysAsnSerProAlaValAlaValValArgThrPhePherIleThrPheAla 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31554
                                                                                                                                                                                                                                                                                                                                      487 SerValMetProThrProLeuArgGlyIleHiSHiSArgThrArgSerProArgLeuAla 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| ::: ||||||| 547 TyrPheLysLeuArgGlyThrLeuLysThrGlnAsp------SerPheGlnValpro 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564 IlePheValProValValPheLeuGlyIleCyslleAlaLeuLeuVallleProileThr 583
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584 GlnAsnTyrHisValAlaIleTyrGLyValSerMetThrIleGlyGlyAlaIleIleTyr 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604 LeullePhellePheProAsnThrLeuProllePheLeuHisLysIleAsnAsnSerIle 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1681 ACCAGAACATTACAAATAATACTGGAAGTTGTA-----CCAGAAGAAGAT 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         624 ValLysPheAlaGlnIlellePheAsnCysVallleGluProTyrGluAsp 640
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A;Cross-references: EMBL:AL117201; PIDN:CAB55063.1; CESP:Y53H1C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Y53H1C.1 - Caenorhabditis elegans
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A; Accession: T31554
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A;Introns: 31/1; 90/3; 127/1; 154/1; 198/1; 249/2; 325/2; 371/2; 433/3; 467/1; 510/1
                                                                                                                                                                                                376 GICTCCATIATCATIGGCACCATCATIGGAGCAGGAATCTICATCICTCCTAAGGGCGTG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           982 CICAACTITGITACIGAAGAAGIAGAAAACCCIGAAAAAACCATICCCCIIGCAAIAIGI 1041
                                                                                                                                                                                                                                                                436 CTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTGTGGGGGTCCTG 495
                                                                                                                                                                                                                                                                                                                                TCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGT 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     766 AATAGCATGAGTGTC-----AGCTGGAGCGCCCGGATCCAGATTTTCTTAACC 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 IleGlyGlnIleSerLeuAlaPheTyrGlyAlaLeuTrpSerPheAlaGlyTrpAspIle 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GAACCATTTTTTTTATGTGAA 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 ATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 814 TTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATT--- 870
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                                                                                                                                                                                                                      26 MetSerTyrValileAlaAsnileIleGlyAlaGlyIlePheIleThrProGlyThrVal 45
                                                                                                                                                                                                                                                                                                                                                   277 LeuAspThrGluThrLeuLysAsnSerSerAlaValAlaAlaAspPheAlaArglleThr 296
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1216 TCCATGAACGGTGTGTTTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGT 1275
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                                                                                                                                                                                                                                                                                                                                                          751 GTAGTGATGGTCCTAAATAGCATGAGTGTC------AGCTGGAGCGCCCGGATC 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 ThrasnProGlyGlnIleSerLeùAlaPheTyrGlyAlaLeuTrpSerPheAlaGlyTrp 244
           517 TATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAA 576
                                    577 GICITIGGICCATIACCAGCITITIGIACGAGICIGGGIGGAACTCCTCATAAIACGCCCI 636
                                                                                                                                    110 ValGlyTrpGluGlyIleAlaPheSerPheMetTrpValGlyValIleMetSerPhePro 129
                                                                                                                                                                                                                                                                                                   404 IleArgTyrArgAsnIleProValHisProAspAlaIleArgValProLeuIlePheSer
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A;Experimental source: strain Bristol N2; clone T13A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 23/2; 107/3; 140/1; 167/1; 211/1; 259/2; 335/2; 381/2; 500/1; 540/1
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                  1282 CCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTT 1341
                                                                                                                                                      1342 TTGCACCCTTTGACAATGATAATGCTCTTCTTGGAGACCTCGACAGTCTTTGAATTTC 1401
                                                                                                                                                                                                                                          1402 CTCAGTTTTGCCAGGTGGCTTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGA 1461
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337 ProThrPheLeuSerCysIleAsnAlaGluSerAsnSerProArgAlaAlaLeuLeuPhe 356
                                                                                                                                                                                               357 GlnLeuIleCysThrIleAlaValThrPheVal---AspThrGluSerLeuIleThrTyr 375
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A; Residues: 1-562 <NEL>
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Qy Dp	1624	C 16
ογ	1684	1719
Q	Db 504 ArgileThrCysLysileLeuPheThrThrProAsp	::: rThrProAsp 515
RESU T248 hypo C;Sp C;Da C;Ac	RESULT 9 T24837 Hypothetical protein T11F9.4 - Caenorhal C:Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 1 C;Accession: T24837	Caenorhabditis elegans ns evision 15-Oct-1999 #text_change 15-Oct-1999
Subm Subm A; Re	Wilennard, N. Submitted to the EMBL Data Library, June Alreference number: 219941	June 1996
A; St A; Mo	F	om GB/EMBL/DDBJ
A; Re A; Cr A; Ex	0 <wil> es: EMBL:274042 ource: clone T1</wil>	; PIDN:CAA98529.1; GSPDB:GN00023; CESP:T11F9.4 1F9
A; Ge A; Ma A; Ma	A/Gene: CISS:T11F9.4 A/Map position: 5 A:Introns: 41/3; 237/2; 269/3; 386/1	
Aligi Pred Score Perce Best Query	ignment Scores: 5.18e-42 Dre: 564.00 ccent Similarity: 48.60% st Local Similarity: 29.25% : 7.50 Match: 13.69%	Length: 440 Matches: 136 Conservative: 90 Mismatches: 159 Indels: 80 Gaps: 10
ns-0	-09-667-170A-440 (1-2239) x T24837 (1	-440)
Oy Dp	352	AGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGA 411 ::: ::: ::
Oy Db	412	ATCTTCATCTCTCTAAGGCCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACC 471 :: IlePhelleThrProThrSerllelleGluAsnValAsnSerlle 42
οy	472	ATCTGGACGGTGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGA 531
යු ,	43	GlnIleGlnGlyAlaGly 48
oy Ob	532 49	A 5
δ	592	C
Op	56	LysLeuLeuGlyPheSerLeulle 68
. YO	. 652	TGTGAAATCCCT
δy	712	GAACTIGCGATCAAGCTCATTACAGCTGTGGGCATAAQTGTAAGTGTAATGTGTTGTAAAAATGT 771
g G	84	

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949 IATGGAATGTATGCATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAA 1008
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                                                                         832 ATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATT---AAAGGTCAAACGCAGAAC 888
                                                                                                   889 ITTAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTAT 948
                                                                                                                                                                                        118 LeuGluGluProPheLysGlySerAsnTrpAsnProGlyProPheValAsnAlaLeuPhe 137
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772 AIGAGIGICAGCIGGAGCGCCCGGAICCAGAITIICTIAACCIITIGCAAGCICACAGCA 831
                                                                                                                                                                                                                                                                                                                                238 TyrLeuGlnAlaValSerArgGlnGlyHis::||| :::||| 1|1
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                                      85 ------ArgPheSerIleLeuAlaSerLeuAlaLysIleAlaAla 97
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377 PheArgAsnAlaThrHisValIleAsnGluGluSerThrLysPheMetGlnIleIlePhe 396
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                        C; Accession: B65855

R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C; Brunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Parorel, S.; Brusilit, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Rumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Koetter, P.; Mulber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oddega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Y, M.; Gawa, R.; Schleich, S.; Schoceter, P.; Toerpstra, P.; Tognoni, A.; Schowska, A.; Seronakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Winters, P.; Winte
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A; Ressidues: 1-4.38 -KUN>
A; Ressidues: 1-4.38 -KUN>
A; Cross-references: GB: 299110; GB: AL009126; NID: 92633472; PIDN: CAB13143.1; PID: 92633640
A; Experimental source: strain 168
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
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Cipecies: Staphylococcus aureus
Cipecies: Staphylococcus aureus
Cipecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Cipecession: B89921
Cipecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Cipecies: 10-May-2001
Cipecies: Mizutani-Ui, Y.; Kobayashi, N.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Cipecies: A; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUID:21311952; PMID:11418146
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A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 ValThrLeuGlyGluAsnAlaThrSerThrAlaAlaThrMetLeuPheGlySerIleGly 276
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                                                                                                                                                                 940 GCTTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAA 999
886 AACTITAAAGACGCCTTITCAGGAAGAGAITCAAGTATTACGCGGTTGCCACTG----- 939
                                                                            179 -----GlnHisIlePheThrAlaValAsnGluSerIleSerAspMetAsnPheGlyAla 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1348 CCTTTGACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGT
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Length: Matches: Conservative: Mismatches: Indels: Gaps:	(1-440)	CAGGAAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCT :: ::: snGlyLysGluLeuGlnLysAsnIleGlyPhePheSerAlaPheA	AATCTTCATCTCTCCTAAG	sIles	ACGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCCTGTCACT :: ::: ::: ::: ThrGlyThralaGlyMetAlaLeuPhevalTrpPheLeuGlyGlyIleIleThrIl	GGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACA	TATATTTGGAAGTCTTTGGTCCATTACCAGGTTTTTTTGGAAGTCTTTTGGAAGTCTTTTTTTT	 TyrileGluTyrThrTyrGlyAspPheTrpGlyPheLeuSerGlyTrpAl	######################################		nicoledancaderratederrathracaerr erleulleproilealailealaserala	GTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGAT	::: GlySerLysAla	ACAGCAATTCTGAT	::::::::::::::::::::::::::::::::::::::	CTAATTAAAGGTCAAACGCAGAACTTTAAAGAC	LeulleProThrThrGl	Ö	-PheThrAlaIleGlySerGlyLeuLeuAl.	AACTTT	ATGTATATCCATGCCATTGTCACCATTCCTATATCCT	valGlyIleGlyCysIleMetAl	ACAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGGTGCTGCTTTCAAAT		- (pheGlyGluAsnGlyGlyLy	ITGTTGCCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTA ::: ::: ::: ::::
1.92e-34 479.50 49.38 7: 27.90%	l-2239) x E89921	NGAAAGTGCAGCTGAA 	ATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCTC :::::: ::: :	alMetGlyThrValIleGlySerGlyValPhePheLy	'GGGCATGTCTCTGAC' ::: aGlyMetAlaLeuPh	GGAGCTTTGTCTTATGCTGAATTGGG 	AGTCTTTGGTCCATT	::: rThrTyrGlyAspPhe	AATACGCCCTGCAGCTACTGCTGTC 		: uSerIleGlySerLeu	FGTAGTGATGGTCCTA	LeuSerIleValLeulleAsnPheLeuGlySerLy	AACCTTTTGCAAGCTC	hrLeuVallleLysLeull		AspileThrPheSerLeuil	AGAGATTCAAGTATT	Phe	ATATGCTGGCTGGTTTTACCTC,	GCAAT	Alail	TACTTTACGACCATT	PheLeuLeuThrLeuProll	TTTCTGAGCGGCTACTG	aSerAspThrSerLysIleLeuPheGl	TCCTGCTTTGGCTCC!
ment Scores: No.: :: Int Similarity: Local Similarity Match:	7-170A-440 (1	3 T	ري ري	0 Valm	n 0	ر د	2	0		5 CCATTTTTATTCAATGTGAA	0 LeuPheHisLeuSerIleGlyS	9 GTGGGCATAAC1	7 LeuSerIleVal	9 CAGATTTTCTTP	GlnSerValT	ATGCAG	Ρh	8 5			AAAAC	-		IleAsnAlaThr	AGT	AlaAlaSerAsp'	TTTGTTGCCCTC:::
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C.Species: Nostoc sp.
A.Note: No
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A;Experimental source: strain PCC 7120
                                                                        1252 TICTATGTTGCGTCTCGAGAGGGTCACCTTCCA-----GAAATCCTCTCCATGATTCAT 1305
                                                                                                                                                                                                                    1306 GTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATG 1365
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286 GlylleLeulleSerValTyrGlyThrIleAsnGlyTyrThrMetThrGlyMetArgVal 305
                                                                                                                                            306 ProTyrAlaMetAlaGluArgLysLeuLeuProPheSerHisLeuPheAlaLysLeu--- 324
                                                                                                                                                                                                                                                                                            325 ThrLysSerGlyAlaProTrpPheGlyAlaIleIleGlnLeuIleIleAlaIleIleMet 344
                                                                                                                                                                                                                                                                                                                                                                                                                 365 TyrCysMetSerPheValAlaValIleIleLeuArgLysArgGluProAsnMetGluArg 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 TIACIGAGGGGAGTCTCCATTATCATIGGCACCATCATIGGAGCAGGAATCTTCATCTT 423
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C; Accession: B69172
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A; Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                              cationic amino acid transporter related protein - Methanobacterium thermoautotrophicu C;Species: Methanobacterium thermoautotrophicum C;Species: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 20-Aug-1999
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A; Cross-references: GB: AE000837; GB: AE000666; NID: 92621613; PIDN: ABB85052.1; PID: 9262
A; Cross-references: GB: AE000837; GB: AE000666; NID: 92621613; PIDN: ABB85052.1; PID: 9262
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C,Superfamily: arginine permease
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A; Molecule type: DNA A; Residues: 1-574 <ENT>

a a	153	ThrIleLeuLysValAlaProValLeuLeuPheAlaValLeuGlyAlaIleHisLeuAla 172
Οý	871	AAAGGTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGAAGA
qq	173	
Qy	913	GATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGG
Q	193	20
oy Dp	973	TGGTTTTACCTCAACTTGGTACTGAAGAAGTAGAAAACCCTGAAAAAACCATTCCCGTT 1032 ::: PheGluLeuValThrValProAlaAspGluValArqAspProGluArgThrIleProfien 226
ΩÝ	1033	
qq	227	246
Oy	1093	TTTACGACCATTAATGCTGAGGAGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCT 1152
g	247	LeuGlyLeuValProTrpArgValLeuAlaSerSerThrAlaProLeuThrValAlaGly 266
à		GAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTGCTGC 1209
a 6		TyrSerLeuMetGlyGlyIleGlyAlaLeuIleLeuThrAlaGlyAlaValPheSerIle 286
3 8	287	TITGGCTCCATGAACGGTGGTGTTTGCTGTCTCCCAGGTTATTCTATGTTGCTCCGA 1269
ì		ricary scretusianda da 17 Met Leurnir Infra da Arg Leureu Pheala Met Ser Glu 306
전		savestracciticcagadatcciccargaricargaricargcacacacacacacacacacacacacacacacacaca
ĉ	1330	076 JAMESTON TOTAL STREET STRE
5 A		octofiativitiveAcceptTGACAATGATAATGCTCTTCTCTGGAGACCTCGACAGT 1389 ::::::::: ::: SerIleLeuvalGlnAsnLeuThrAlaLeuLeualaAlaLeuThrGlyThrValSerGly 346
٥y	1390	
Ω	347	366
δŏ	1450 /	
QQ	367	3
οy	1510 (15
qq	386	397
Qy	1570 1	TTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTT 1629
Op	398	SerThrThrAlaTrpGlyLeuLeuLeu1leLeuSerGlyAlaProLeuTyrLeu1lePhe 417
RESU S619 meth N;Al	LT 14 43 ionine ternate ecies:	ns ns
C; Da	te: 10- cession	Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000 1: S61943; S64349
R; IS Subm	nard, A itted t	N.D.; Thomas, D.; Surdin-Kerjan, Y.
A; Re	terence cession	: number: \$61943 :: :561943
A; Re	sidues:	Lype: DNA 1-574 <isn></isn>
A; EX	perimen	erences: EMBL:U40316; NID:g1101906; PIDN:AAB63529.1; PID:g1101907 tal source: strain X2180-1A
Subm	itted t farence	D.; KoSe, M.; Koetter, P.; Roehmer, A.; Sehrsam, I.; Hempel, S. o the Protein Sequence Database, May 1996
A; ACC	serence Session	: number: S64335

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A;Cross-references: EMBL:272840; NID:91323066; PIDN:CAA97055.1; PID:91323067; MIPS:YG
A;Experimental source: strain $288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 GACGCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGGCGCCTTTTCAGGAAGAGAAAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 GIGCAGCIGAAGAGGAAAGICACTITACTGAGGGGAGTCTCCAITATCATIGGCACCAIC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 ATTGGAGCAGGAATCTTCATCTCCTAAGGGGGTGCTCCAGAACACGGGCAGCGTGGGC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 ATGTCTCTGACCATCTGGACGGTGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCTTAT 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         520 GCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTC 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 PheArgLys--ProLysPhe------140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700 TGTGAAATCCCT-----GAACTTGCGATCAAGCTCATTACAGCT----- 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 TrpalaalaGlyAsnSerIleAsnThrAlaIleMetPheLeuThralaAlaAspThrGlu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739 ------ATGGTCCTA 765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 AspGlnGlyGluLysGlnLeuGlyIleLeuSerCysIleGlyLeuIleCysAsnArgMet 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 LeuGlyThrGlyValPheAlaValSerSerThrIleTyrThrLeuCysGlySerValGly 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                766 AAIAGCAIGAGIGICAGCIGGAGCGCCCGGAICCAGAITIICIIAACCITIIGCAAGCIC 825
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195 AsnSerLeuAsnValLysIleGlyLeuTyrLeuGlnAsnIleLeuGlyllePheLysIle 214
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                                                                                                    A;Gene: SGD: MUP1
A;Cross-references: SGD:SO003287; MIPS:YGR055w
A;Map position: 7R
C;Superfamily: hypothetical protein YHL036w
C;Reywords: amino acid transport; transmembrane protein
F;92-108/Domain: transmembrane #status predicted <TMA1>F;140-156/Domain: transmembrane #status predicted <TMA2>F;188-199/Domain: transmembrane #status predicted <TMA2>F;280-224/Domain: transmembrane #status predicted <TMA3>F;286-312/Domain: transmembrane #status predicted <TMA5>F;286-312/Domain: transmembrane #status predicted <TMA5>F;396-310/Domain: transmembrane #status predicted <TM5>F;390-406/Domain: transmembrane #status predicted <TM5>F;390-406/Domain: transmembrane #status predicted <TM9>F;457-473/Domain: transmembrane #status predicted <TM9>F;487-473/Domain: transmembrane #status predicted <TM10>F;487-473/Domain: transmembr
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Mismatches:
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Score: 368.50
Percent Similarity: 45.61%
Best Local Similarity: 25.76%
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D87396
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid permease family protein CC1184 [imported] - Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCTTTTG---AATTTCCTCAGTTTTGCCAGGTGGCTTTTTTTTGGGCTGGCAGTTGCT 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TCCCTCTATTCGGAC---CCATTT----- 1572
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1108 GCTGAGGAGCTGCTTTCAAATGCAGTG---GCAGTGACCTTTTCTGAGCGGCTACTG 1164
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                                                                                                                                                                                                                                      988 ITTGTTACTGAAGAAGTAGAAAACCCTGAAAAACCATTCCCCTTGCAATATGTATATCC 1047
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                                                                                                                                                                                                                                                                  295 MetValPheLeuAlaileIleTyrilePheValAsnileAlaTyrPheAlaValValPro 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 LysAspLysLeulleSerSerLysLeulleLeuAlaAlaAspPhePheAspIleValPhe 334
                                                                                                                                             255 GlylleValAsnAlaLeuTyrSerValIleTrpSerPheValGlyTyrSerAsnValAsn 274
                                                                                   215 GlylleValLeuPhelleSerlleThrGlyTrpValAlaLeuGlyGlyGlyLeuLysAsp 234
                                                  877 -----CAAACGCAGAACTTTAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACG--- 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1675 AAAATA 1680
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B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; K. n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, J. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A.Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-546 <STO>
                                                                                                                                                                      A; Cross-references: GB: AE005673; NID: 913422508; PIDN: AAK23168.1; GSPDB: GN00148
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 aprometTrpAlaThrProLeuIleGlnAlaValAlaAlaAroGlyGlyGlyThrMetPh 188
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248 SPTOPHEILEPROGLUPTOTHEGLGIN———ATGTATCCAATAGEGGGGGGGGGGGGGGGGGGGGGGGGGG

Search completed: April 16, 2003, 16:26:07 Job time: 65 secs

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(without alignments)
7429.240 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                   OM nucleic - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                     112892 seqs, 41476328 residues
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Maximum Match 100%
Listing first 45 summaries
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Command line parameters:

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMARIES	
Result		Query				
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1	2519	61.1	501		XCT HIMAN	
7	2307	56.0	502	-	XCT MOTISE	Ogupyo nomo sapien
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9	1131.5	27.5	511	- ۱	VIAL MOUSE	Q9z127 mus musculu
7	1108	26.90	533	٦.	ILAI_HUMAN	Q9um01 homo sapien
80	1103	26.90	, c	4 -	LAIZ_KAI	
6	1101.5	26.5	100	٦.	LATZ_MOUSE	Q9qxw9 mus musculu
10	1075.5	26.7	100	- ۱	Dami mman	Q9uhi5 homo sapien
11	1074.5	26.1	707	- ا	DAIL HUMAN	P82251 homo sapien
12	1067.5	25.0	7 7	٦.	DAII_KAT	P82252 rattus norv
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18	286		900	٠,	CTRZ_HUMAN	P52569 homo sapien
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P30825 homo sapien

Q09143 mus musculu P30823 rattus norv P18581 mus musculu P71400 escherichia		P7737 escherichia Q47689 escherichia P18656 emericella Q58026 methanococc P37460 salmonella Q10875 mycobacteri P24170 escherichia chia		P25737 escherichia P22891 escherichia P39269 escherichia P48813 saccharomyc
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 TITICAGGAAGAGACGCCTTTTCAGGAAGAGAAAGTGCAGCTGAAGAGGAAAGTCACT 363
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                                                        SUBDIVIT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACID TRANSPORT PROTEIN SLC3A2/4F2HC (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein (Probable).
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 CTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACGCC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY EXCHANGE OF ANIONIC
AMINO ACIDS WITH HIGH SPECIFICITY FOR ANIONIC FORM OF CYSTINE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .) (POTENTIAL).
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Mismatches:
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InterPro; IPR004760; L_AA_transport.
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TIGRFAMS; TIGR00911; 2A0308; 1.
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EMBL; AF200708; AAG35592.1; -.
EMBL; AF252872; AAK49111.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                 1624 CTCTTTATATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACC 1683
-1- SUBUNTT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACID TRANSPORT PROTEIN SLC3AZ/4F2HG.
-1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cystine/glutamate transporter (Amino acid transport system xc-) (xCT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=129/SvJ; TISSUE=Liver;
Sasaki H., Sato H., Bannai S.;
"Isolation and functional characterization of mouse cystine/glutamate
exchange transporter gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY EXCHANGE OF ANIONIC AMINO ACIDS WITH HIGH SPECIFICITY FOR ANIONIC FORM OF CYSTINE AND
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato H., Tamba M., Ishii T., Bannai S.; "Cloning and expression of a plasma membrane cystine/glutamate exchange transporter composed of two distinct proteins."; J. Biol. Chem. 274:11455-11458(1999).
                                                                                                                                                                        1684 AGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAAGATAAGTTA 1731
                                                                                                                                                                                         PRT;
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EMBL; AB037661; BAA90522.1; -.
EMBL; AB037650; BAA90522.1; JOINED.
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BAA90522.1; BAA90522.1; BAA90522.1;

AB037658; AB037659; AB037660;

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184 AAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGAGG 243
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         InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004760; LAA_transport.
InterPro; IPR004841; Permeases.
Pfam: PF00324; aa_permeases; 1.
TIGRRAMS; TIGR00911; 2A0308; 1.
TRANSPORT; AMINO-acid transport; Transmembrane.
TRANSMEM 44 64 POTEWIAL.
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 MGI:1347355;
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                       844 ATAGICCCIGGAGITAIGCAGCIAAITAAAGGICAAACGCAGAACITIAAAGACGCCIII 903
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Q01650; Q9UBNB; Q9UPL5; Q9UQCO;
01.UUN-1994 (Rel. 29, Created).
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
16-OCT-2010 (Rel. 40, Last annotation argants)
16-OCT-2010 (Rel. 40, Las
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

MEDLINE=99172172; PubMed=10072483;

Tsurudome M., Ito M., Takebayashi S., Okumura K., Nishio M.,

Tsurudome M., Kusagawa S., Komada H., Ito Y.;

"Primary structure of the light chain of fusion regulatory protein-
"[CD98/4F2 predicts a protein with multiple transmembrane domains that is almost identical to the amino acid transporter El6.";

J. Immunol. 162:2462-2466(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -; - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                                                                                                                      Mastroberardino L., Spindler B., Pfeiffer R., Skelly P.J., Loffing J., Shoemaker C.B., Verrey F.; "Amino-acid transport by heterodimers of 4F2hc/CD98 and members of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-:- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN ADULT LUNG AND LIVER,
AND IS ALSO EXPRESSED IN BRAIN, THYMUS, RETINA AND SOME OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Human LAII, a subunit of system L amino acid transporter: molecular cloning and transport function."; Biochem. Biophys. Res. Commun. 255:283-288(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prasad P.D., Wang H., Huang W., Kekuda R., Rajan D.P., Leibach F.H.,
Ganapathy V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A novel transiently expressed, integral membrane protein linked to cell activation. Molecular cloning via the rapid degradation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 267:11267-11273(1992).
-!- FUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY TRANSPORT OF LARGE NEUTRAL AMINO ACIDS. INVOLVED IN CELLULAR AMINO ACID UPPAKE.
-!- SUBUNIT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACID
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                               IISSUE-Ovary;
Yanagida O., Segawa H., Miyamoto K., Takeda E., Goya T., Endou
                                                                                                                                                                                                                                                                                                                                            'Cloning and characterization of a human system L amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minato N., Iwai K., Takizawa C., Nakamura E.; "Human 4F2 light chain: amino acid transporter."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Peripheral blood lymphocytes;
MEDLINE-92283834; PubMed=1597461;
Gaugitsch H.W., Prieschl E.E., Kalthoff F., Huber N.E.,
                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
chain) (Integral membrane protein E16) (hLAT1).
SLC7A5 OR LAT1 OR MPE16 OR CD98LC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
MEDLINE=99160855; PubMed=10049700;
                                                                                                                                            MEDLINE=98421678; PubMed=9751058;
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Nature 395:288-291(1998).
                                    Homo sapiens (Human)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/

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247 CCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACGCCTTT 306
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N -> K (IN REF. 1).

N -> K (IN REF. 1).
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InterPro; IPR004841; Permease.
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TIGRFAMS; TIGR00911; 2A0308; 1.
                     EMBL; AF077866; AAC61479.1; -. EMBL; AB018009; BAA84648.1; -.
                                                    EMBL; AB018542; BAA33851.1;
EMBL; AB017908; BAA75746.1;
EMBL; M80244; AAA35780.1;
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113 SerGlyGlyAspTyrAlaTyrMetLeuGluValTyrGlySerLeuProAlaPheLeuLys 132
                                 607 GICTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGCATTT 666
                                                                                                     667 GGACGCTACATTCTGGAACCATTTTTTATTCAATGTGAAATCCCTGAACTTGCGATCAAG 726
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Hepatona;

MEDILINE-5511385; Pubmed=7532544;

MEDILINE-5511385; Pubmed=7532544;

A REDLINE-5511385; Pubmed=7532544;

TAAI, a highly conserved oncofetal complementary DNA from rat hepatoma, encodes an integral membrane protein associated with liver development, carcinogenesis, and cell activation.";

Tanoment, carcinogenesis, and cell activation.";

Cancer Res. 55:1152-1159(1995).

Cancer Res. 55:1152-1159(1995).

Cancer Res. 55:1152-1159(1995).

TRANSPORT ANINO ACIDS. INVOLVED IN CELLULAR AMINO ACID UPTAKE.

TRANSPORT PROTEIN SLC3A24F2HC.

TRANSPORT PROTEIN SLC3A24F2HC.

TRANSPORT PROTEIN INTEGRESSED HEBATOWA BUT NOT IN NORMAL LIVER.

C. - SUBGELLULAR EXPRESSED HEBATOWA BUT NOT IN NORMAL LIVER.

ALSO EXPRESSED IN PLACENTA, TESTIS, BRAIN, OVARY, SPLEEN, MANMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                               LAT1_RAT STANDARD; PRT; 512 AA.
063015; Q90WL4;
010-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 Lg) (Integral membrane protein E16) (TA1 protein).
                                                                                                                                                                                                                                                                                                                                                          Kanai Y., Segawa H., Miyamoto K., Uchino H., Takeda E., Endou H.; "Expression cloning and characterization of a transporter for large neutral amino acids activated by the heavy chain of 4F2 antigen
                  1681 ACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAA 1722
                                !ransport; Amino-acid transport; Transmembrane.
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InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004760; L_AA_transport.
InterPro; IPR0044841; Permease.
                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 273:23629-23632(1998).
                                                                                                                                                                                                                                                                                                                                             MEDLINE=98395066; PubMed=9726963;
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TIGRFAMS; TIGR00911; 2A0308; 1.
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1060 ACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTG 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 778 GTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTG 837
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                                                  POTENTIAL.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

B487CE0B58D73A02 CRC64;
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67.578
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512 AA;
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1120 CTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTA 1179
                                                           1180 GCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCT 1239
                                                                                                                       1240 GTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATG 1299
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                391 MetTyralaPheSerargAspIlePheSerIleIleAsnPhePheSerPhePheAsnTrp 410
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16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Large neutral amino acids transporter small subunit 1 (L-type amino acid transporter 1) (4F2 Ight chain) (4F2 LC) (4F2LC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura E., Sato M., Yang H., Miyagawa F., Harasaki M., Tomita K., Matsuoka S., Noma A., Iwai K., Minato N.; Harasaki M., Tomita K., 4F2 (CD98) heavy chain is associated covalently with an amino acid transporter and controls intracellular trafficking and membrane topology of 4F2 heterodimer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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"Localization of expression of system L neutral amino acid transporter
                                                                                                                      -!- SIMILARITY: BELONGS TO A FÁMILY THAT GROUPS MANY AMINO ACID PERWEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
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              LATI in brain.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY TRANSPORT OF LARGE NEUTRAL AMINO ACIDS. INVOLVED IN CELULAR AMINO ACID UPPAKE.
-!- SUBUNIT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                        TRANSPORT PROTEIN SLC3A2/4F2HC.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Transport; Amino-acid transport; Transm
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TIGREAMS; TIGR00911; 2A0308; 1.
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                                                                                                                      CIGGCATIIGGACGCIACATICIGGAACCATITITITITITATICAAIGIGAAAICCCIGAACTI 717
                                                                                                                                                                                                                                                                    151 LeuValPheAlaThrTyrLeuLeuLysProValPheProThrCysProValProGluGlu 170
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                       111 ileSerLysSerGlyGlyAspTyrAlaTyrMetLeuGluValTyrGlySerLeuProAla 130
                                                                                  598 ITTGTACGAGICIGGGIGGAACTCCICATAATACGCCCTGCAGCIACIGCIGIGAIAICC 657
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Torrents D., Estevez R., Pineda M., Fernandez E., Lloberas J., Shi Y.-B., Zorzano A., Palachn M.; Identification and characterization of a membrane protein (y+L amino acid transporter-1) that associates with 4F2hc to encode the amino acid transport activity y+L. A candidate gene for lysinuric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99178268; PubMed-10080183; BASIA M.T., Sperandeo M.P., De Grandi A., Buoninconti A., Riboni M., Manzoni M., Incerti B., Pepe A., Andria G., Ballabio A., Sebastio G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Takayama K., Yoshimoto M.;
"Molecular and bological characterization of a novel monocyte amino
"Molecular and MOP-2.";
acid permease, MOP-2.";
                                   1660 AGAATAATGTCAGAAAAAAAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAA 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "SLC7A7, encoding a putative permease-related protein, is mutated in patients with lysinuric protein intolerance."; Nat. Genet. 21:297-301(1999).
                                                       491 LeuGlnAla1lePheSerValThrValLeuCysGlnLysLeuMetGlnValValProGln 510
471 LeuSerGlyLeuProValTyrPhePheGlyValTrpTrpLysAsnLysProLysTrpIle 490
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MEDLINE=20202147., Koizumi A., Takahashi T., Shoji Y.,

Matsumori M., Kayo T., Ohata T., Wada Y., Yoshimura I., Maisawa S.,

Konishi M., Takasago Y., Takakada G.;

"SLC7A7 genomic structure and novel variants in three Japanese

Hysinuric protein intolerance families.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfeiffer R., Rossier G., Spindler B., Meier C., Kuhn L., Verrey F.; "Amino acid transport G, Y-L-type by heterodimers of 4F2hc/CD98 and members of the glycoprotein-associated amino acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fukasawa Y., Segawa H., Endou H., Kanai Y.; "Characterization of a human system y+L amino acid transporters."; Submitted (NoV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                         Y+L amino acid transporter 1 (y(+)L-type amino acid transporter 1) (y+LAI-1) (x+LAI1) (Monocyte amino acid permease 2) (MOP-2).
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11)
MEDINECE FROM N.A., AND VARIANT LPI ARG-334.
MEDINE-99047611; PubMed-9829974;
TORTENTS D., Estevez R., Pineda M., Fernandez E., Lloberas J.,
                                                                                                                                                                                                                                     YLA1_HUMAN STANDARD; PRT; 511 AA. 09DMO1; 09P2V5; 095984; 16-007-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 273:32437-32445(1998).
                                                                                                                                                                                                                                   PRT;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEUTRAL AMINO ACIDS.

1- SUBJUNT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACID TRANSPORT PROTEIN SICJAZ/AFZHC.

1- SUBGELLULAR LOCATION: Integral membrane protein (Probable).

1- SUBCELLULAR LOCATION: INTEGRAL BLOOD LEUKOCYTES >> LUNG >> PERIPHERAL BLOOD LEUKOCYTES >> PERIPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALVECLAR PROTEINOSIS) ARE ALSO SEEN. BIOCHEMICALLY LPI IS CHARACTERIZED BY A DEFECT IN THE PLASMA MEMBRANE TRANSPORT OF DIBASIC AMINO ACIDS.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE-20122253; Wilder 1065553; Wilder 20122253; Warkaenen J., Torrents D., Pineda M., Camps M., Yoldi M.E., Horell - Kuitunen N., Huoponen K., Heinonen M., Oksanen J., Simell O., Savontaus M.-L., Zorzano A., Palacin M., Aula P.; Functional analysis of novel mutations in y+LAT-1 amino acid transporter gene causing lysinuric protein intolerance (LPI)."; Hum. Mol. Genet. 9:431-438(2000).
                                                                                                                                                                                                                    Sperandeo M.P., Bassi M.T., Riboni M., Parenti G., Buoninconti A., Manzoni M., Incerti B., Larocca M.R., Di Rocco M., Strisciuglio P., Sabastio G., Borsani G., Schastio G., Ballabio A., Andria G., Structure of the SLC7A7 gene and mutational analysis of patients Am. J. Hum. Genet. 66:92-99(2000).
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                     Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                               MEDLINE-20100611; PubMed=10631139;
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BAA95120.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS LPI VAL-54 AND ASP-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ130718; CAA10198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF092032; AAC83706.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y18474; CAB40136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB020532; BAA87623.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAA95120.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C003062; AAH03062.1;
C010107; AAH10107.1;
HGNC:11065; SLC7A7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAA95120.1;
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                                                                                                                                                                     VARIANT LPI ARG-386
                                                 SEQUENCE FROM N.A.
                                                                         FISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB031531;
                                                                                                      Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB031536;
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MIM; 222700;
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310 GGAAGAGGCCTTTTCAGGAAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTG 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      550 GGAGGTCATTACACATATATTTGGAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610 TGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGA 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             730 ATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGC 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           790 GCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATAATTATAGTC 849
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         Pfam; PF00324; aa_permeases; l.
Transport; Amino-acid transport; Transmembrane; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490 GTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCT
                                                                                                                                                                                                      G -> D (IN LPI).

/FIId=VAR_010999.

S -> R (IN LPI).

/FIId=VAR_011000.

A -> V (IN REF. 4).

W; A71D677B6B075894 CRC64;
                                                                                                                                                                                                                                                                                                                     149
                                                                                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                   L -> R (IN LPI). /FTId=VAR_010262.
                                                                                                                                                                          /FTId=VAR_010261
                                                                                                                                                                                                                                                                                                                     Mismatches:
                                                                                                                                                                  (IN LPI)
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55990 MW;
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45.05%
27.46%
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89
127
153
180
206
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Best Local Similarity:
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1570 TTTAGTACAGGGATTGGCTTCGTCATCACTGGAGTCCCTGCGTATTATCTCTTT 1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1510 CCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCA 1569
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                         1150 TCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGC 1209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 IleAsnSerLeulleGly11eAla11eAlaLeuSerGlyLeuProPheTyrPheLeulle 460
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                                                                                                                                                                                                                 1030 CTIGCAATAIGIATAICCAIGGCCAIIGICACCAIIGGCIAIGIGCIGACAAAIGIGGCC 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 SerLeuLeuPheAsnGlyIleMetAlaLeuIleTyrLeuCysValGluAspIlePheGln 380
                                                                                                                                         970 GGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCTGAAAAAACCATTCCC 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AlaAspGlnIlePheGlyIlePheAsnTrpIleIleProLeuSerValAlaLeuSerCys 320
                                                                                                                                                              221 SerSerPheAlaValGlyAspIleAlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSer 240
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16-OCT-2001 (Rel. 40, Last amotation update)
Large neutral amino acids transporter small subunit 2 (L-type amino acid transporter 2).
850 CCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAAGACGCCTTTTCAGGA 909
                                201 AlaGly11eValArgLeuGlyGlnGlyAlaSerThrHisPheGluAsnSerPheGluGly 220
                                                                     910 AGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTATGCATATGCT 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1684 AGAACATTACAAATAATA---CTGGAAGTTGTACCAGAAGAAGAT 1725
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                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 AITAICAITGGCACCAICAITGGAGCAGGAAICTICAICTCCTAAGGGGGGTGCICCAG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 TITICAGGAAGAGAAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 AAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGACGCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 ATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGAGGCTGCCTTCCCTGGGCAAC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----valAlaLeuLysLysGluIleGlyLeuValSerAlaCysGly 48
                                                              Segawa H., Fukasawa Y., Miyamoto K., Takeda E., Endou H., Kanai Y.; Segawa H., Fukasawa Y., Miyamoto K., Takeda E., Endou H., Kanai Y.; Segawa H., Fukasawa Y., Miyamoto K., Takeda Substrate selectivity."; neutral amino acid transporter with broad substrate selectivity."; J. Biol. Chem. 274:19745-19751(1999)

J. Biol. Chem. 274:19745-19751(1999)

I. FUKUTION: SODIUM-INDEPENDENT, HIGH-AFFINITY TRANSPORT OF LARGE NEUTRAL AMINO ACIDS. HAS TRANSPORTED AT PHYSIOLOGICAL CONCENTRAIONS. LATI L.-ALANINE IS TRANSPORTED AT PHYSIOLOGICAL CONCENTRAIONS. PLAYS A ROLE IN BASOLATERAL (RE) ABSORPTION OF NEUTRAL AMINO ACIDS.
                                                                                                                                                                                                                                                                  PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 AspThrSerProGluAlaGluAlaSerSerGlyGlyGlyGly------ 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetGluLysGlyThrArgGlnArgAsnAsnThrAlaLysAsnHisProAspArgGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein (Probable). SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99479DB60DA69DF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533
224
100
168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transport; Amino-acid transport; Transmembrane.
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Matches:
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InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004760; L_AA_transport.
InterPro; IPR004841; Permease.
                                                                                                                                                                                                                            TRANSPORT PROTEIN SLC3A2/4F2HC.
                                             TISSUE=Small intestine;
MEDLINE=99321902; PubMed=10391916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00324; aa_permeases; 1.
TIGRFAMS; TIGR00911; 2A0308; 1.
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                                SEQUENCE FROM N.A.
NCBI_TaxID=10116;
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442 AACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCCTGTCACTA 501
                                                                                                     502 TITGGAGCITIGICITATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTAC 561
                                                                                                                                                                                                          109 SerTyrValLysAspIlePheGlyGlyLeuAlaGlyPheLeuArgLeuTrpIleAlaVal 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         964 TATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAAACCCTGAAAAAACC 1023
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49 IlelleValGlyAsnIleIleGlySerGlyIlePheValSerProLysGlyValLeuGlu 68
                                                                                                                                                                                                                                                                                                                                                                                    742 GGCATAACTGTAGTGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAG 801
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                                                        802 ATTITCTTAACCTTTTGCAAGCTCACAGCAATTCTGATAATTALAGTCCCTGGAGTTATG 861
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
1504 TICAICCCAGCTITGTTITCCTICACATGCCTCTTCATGGTTGCCTTTCCCTCTATTCG 1563
                                                                                1564 GACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATTAT 1623
                                                                                                                                                             1624 CTCTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACC 1683
                                         426 LeuPheProlleIleTyrLeuLeuPheTrpAlaPheLeuLeuIlePheSerLeuTrpSer 445
                                                                                                                       446 GluProValValCysGlyIleGlyLeuAlaileMetLeuThrGlyValProValTyrPhe 465
                                                                                                                                                                                          AMILIO GLIAGO ALLO LEGIONE DE LA GENERAL DE LA GENERAL DE LA GENORIOS 62.297-303 (1999).

- I - FUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY TRANSPORT OF LARGE NEUTRAL AMINO ACIDS. HAS HIGHER AFFINITY FOR L-PHENYLALANINE THAT LATIL. L-LAININE IS TRANSPORTED AT PHYSTOLOGICAL CONCENTRATIONS.

- I - SUBUNIT: DISULFIDE-LINEED HEFFRODIMER WITH THE AMINO ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN KIDNEY AND INTESTINE.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "LAT2, a new basolateral 4F2hc/CD98-associated amino acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bassi M.T., Sperandeo M.P., Incerti B., Bulfone A., Pepe A.,
Surace E.M., Gattuso C., de Grandi A., Buoninconti A., Riboni M.,
Manzoni M., Andria G., Ballabio A., Borsani G., Sebastio G.,
"SLC7A8, a gene mapping within the lysinuric protein intolerance
critical region, encodes a new member of the glycoprotein-associated
                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Large neutral amino acids transporter small subunit 2 (L-type amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Embryo;
MEDLINE-20044753; PubMed=10574970;
Rossier G., Meier C., Bauch C., Summa V., Sordat B., Verrey F.,
                                                                                                                                                                                                                                              1684 AGAACATTACAAATAATACTGGAAGTTGTA---CCAGAAGAA 1722
                                                                                                                                                                                                                                                                                    486 LeuValSerGlnLysMetCysValValValTyrProGlnGlu 499
                                                                                                                                                                                                                                                                                                                                                                               531 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of kidney and intestine.";
J. Biol. Chem. 274:34948-34954(1999).
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MEDLINE=20079165; PubMed=10610726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid transporter family.";
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                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transporter 2).
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EMBL; Y19022; CAB69072.1; MGD; MGI:1355323; Slc7a8.

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187 AspilePherhrAlaGlyLysLeuLeuAlaLeuAlaLeuIleIleIleHerdlylleVal 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               802 ATTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATG 861
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                                                                                                                                                                                                                                                                                                                                                                                                                 262 AAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGACGCCTTTTCAGGAAGAGACGCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 ITTTCAGGAAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 AsnalaGlySerValGlyLeuAlaLeulleValTrpIleValThrGlyIleIleThrAla 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LysAsnHisProGlySerAspThrSerProGluAlaGluAlaSerSerGlyGlyGlyGly
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                                                                                                                                                                                                                                                                                                                      Conservative:
                                                                      transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                      Mismatches:
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Matches:
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IPR002293; AA/rel_prmeasel.
IPR004760; L_AA_transport.
IPR004841; Permease.
                                        Pfam; PF00324; aa_permeases; 1.
TIGRFAMS; TIGR00911; 2A0308; 1.
                                                                                                                                                                                                                                                       57873 MW;
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1103.00
64.578
44.538
26.778
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174
208
250
287
329
381
407
                                                                       Transport; Amino-acid
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
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188
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1624 CTCTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACC 1683
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                                                                                                                                                                                                                               1144 ACCTITICTGAGCGGCTACTGGGAAATITCTCATTAGCAGTTCCGATCTTTGTTGCCCTC 1203
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                                                                                                                 1024 ATTCCCCTTGCAATATGTATTCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAAT 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAT2_HUMAN STANDARD; PRT; 535 AA.

LAT2_HUMAN STANDARD; O9UKG7; O9UKG8;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
Large neutral amino acids transporter small subunit 2 (L-type amino acid transporter 2) (hLAT2).
907 GGA---AGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTATGCA 963
                           224 AsnPheGlnGluProAsplieGlyLeuValAlaLeuAlaPheLeuGlnGlySerPheAla 243
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1684 AGAACATTACAAATAATACTGGAAGTTGTA---CCAGAAGAA 1722
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of renal proximal tubule."

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

FUNCTION: SODIUM-THDEPRNDENT, HIGH-AFFINITY TRANSPORT OF LARGE INTITY FOR L-PHENYLALANINE THAT PLAYS A ROLE IN BASCLATERAL (RE)ABSORPTION OF NEUTRAL AMINO ACIDS.

FLAND TO THE STORE HEAD HETERODIMER WITH THE AMINO ACID TRANSPORT PROTEIN SLC3A2/4F2HC.

SUBGLIGHTAR LOCATION: Integral membrane protein (Probable).

TISSUE SPECIFICITY: MAINLY EXPRESSED IN KIDNEY AND INTESTINE.

SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID PERMEASES.
                                                                                            LAT2, a new basolateral 4F2hc/CD98-associated amino acid transporter
                                                                                                                                                                                                                                                                                                                        Borsani G., Bassi M.T., Sperandeo M.P., De Grandi A., Buoninconti A.,
Riboni M., Manzoni M., Incerti B., Pepe A., Andria G., Ballabio A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99321901; PubMed=10391915;
Pineda M., Fernandez E., Torrents D., Estevez R., Lopez C., Camps M., Lloberss J., Zorzano A., Palacin M., "Identification of a membrane protein, LAT-2, that co-expresses with 4F2 heavy chain, an L-type amino acid transport activity with broad specificity for small and large zwitterionic amino acids.";
J. Biol. Chem. 274:19738-19744(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                            "SLC7A7, encoding a putative permease-related protein, is mutated in patients with lysinuric protein intolerance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim D.-K., Fukushima J., Segawa H., Cha S.-H., Chairoungdua A., Matsuo H., Kim J.-Y., Goya T., Endou H., Kanai Y., "Molecular cloning and characterization of a human Na+-independent neutral amino acid transporter expressed in the basolateral membrane
                                  Rossier G., Meier C., Bauch C., Summa V., Sordat B., Verrey F.,
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                                                                                                                               kidney and intestine.";
Biol. Chem. 274:34948-34954(1999).
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InterPro; IPR004841; Permease.
                                                                                                                                                                                                                                                                                             MEDLINE-99178268; PubMed-10080183;
   MEDLINE=20044753; PubMed=10574970;
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TIGRFAMS; TIGR00911; 2A0308; 1.
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EMBL, AF135830; AAF05697.1; --
EMBL, AF135829; AAF05696.1; --
EMBL, AF135828; AAF05695.1; --
EMBL, AB037669; BAB21519.1; --
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                                                                                                                                                                                                                                                              TISSUE=Placenta;
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RANGE STATES STA
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262 AAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGGCCCTTTTCAGGAAGAAGACGCC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 ACATATTTTGGAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTC
                                                                                                                                               AC129146353F1E47 CRC64;
                                                                                                    N -> D (IN REF. 2).
V -> G (IN REF. 2).
G -> R (IN REF. 3).
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Feliubadalo L., Font M., Purroy J., Rousaud F., Estivill X., Nunes V., Golomb E., Centola M., Aksentijevich I., Kreiss Y., Goldman B., Pras M., Kastner D.L., Pras E., Gasparini P., Bisceglia L., Beccia E., Gallucci M., De Sanctis L., Ponzone A., Rizzoni G.F., Zelante L., Bassi M.T., George A.L. Jr., Manzoni M., De Grandi A., Riboni M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1633 ATATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACCAGAACATTA 1692
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1033 GCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAATGTGGGCCTAC 1092
                                                                                          1093 ITTACGACCATTAATGCTGAGGAGCTGCTGTTCAAATGCAGTGGCAGTGACCTTTTCT 1152
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                                                                                                                                                                                                                             308 GluLysLeuLeuGlyValMetAlaTrpIleMetProIleSerValAlaLeuSerThrPhe 327
                                                                                                                                                                                                                                                                                                                       328 GlyGlyValAsnGlySerLeuPheThrSerSerArgLeuPhePheAlaGlyAlaArgGlu 347
                             288 ValThrAlaMetSerProGlnGluLeuLeuAlaSerAsnAlaValAlaValThrPheGly 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
810.4)-Type amino acid transporter 1 (B(0.+)AT) (Glycoprotein-associated amino acid transporter b0,+AT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1693 CAAATAATACTGGAAGTTGTA---CCAGAAGAAGATAAG 1728
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Strausberg R.;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the HGH-APFINITY, SODIUM-INDEPENDENT TRANSPORT OF CYSTINE AND DIBASIC AMINO ACIDS (SYSTEM TRANSPORT OF CYSTINE IN THE RESPONSIBLE FOR THE HIGH-BG()+)-LIKE ACTIVITY). THOUGHT FO BE RESPONSIBLE FOR THE HIGH-BG()+)-LIKE ACTIVITY REABSORPTION OF CYSTINE IN THE AMINO ACID TRANSPORT PORTED SICARA.

SUBMINIT: DISULEIDE-LINRED HETERODIMER WITH THE AMINO ACID TRANSPORT DECELULAR LOCATION: Integral membrane protein (Probable).

TRANSPORT PORTED SICARA SMALL INTESTINE, LIVER AND PLACENTA.

TEAGUE SPECIFICITY: KIDNEY, SMALL INTESTINE, LIVER AND PLACENTA.

TRANSPORT OF CYSTINE AND DIBASIC AMINO ACIDS THROUGH TRACT THREE TYPES OF CYSTINE AND DIBASIC AMINO ACIDS THROUGH TRACT TYPES OF CYSTINE AND DIBASIC AMINO ACID SICARA ARE ASSOCIATED WITH TYPE III CYSTINURIA (CSNU3).

SICARA ARE ASSOCIATED WITH TYPE III CYSTINURIA (CSNU3).

CHERMEASES GIYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                 Pfeiffer R., Loffing J., Rossier G., Bauch C., Meier C., Eggermann T.,
Loffing-Cueni D., Kuehn L.C., Verrey F.;
"Luminal heterodimeric amino acid transporter defective in
Endsley J.K., Ballabio A., Borsani G., Reig N., Fernandez E.,
Estevez R., Pineda M., Torrents D., Camps M., Lloberas J., Zorzano A.,
                                                                                                                                                                                                                                                                                                                                                                                                    "Human cystinuria-related transporter: localization and functional characterization.";
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Amino-acid transport; Transmembrane; Disease mutation.
                                              Palacin M.; "Non-type I cystinuria caused by mutations in SLC7A9, encoding
                                                                                                                                                                                                                                                                                                                                                 Mizoguchi K., Cha S.H., Chairoungdua A., Kim J.Y., Shigeta Y., Matsuo H., Fukushima J., Awa Y., Akakura K., Goya T., Ito H., Endou H., Kanai Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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Interpro; IPR004841; Permease.
                                                                                                                                                                                                                                                                Mol. Biol. Cell 10:4135-4147(1999).
                                                                                                                                                            TISSUE=Kidney;
MEDLINE=20056095; PubMed=10588648;
                                                                                                                                                                                                                                                                                                                                      MEDLINE=21219147; PubMed=11318953;
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EMBL; AJ249199; CAB54003.1; -.
EMBL; ARD33548; BAB16840.1; -.
EMBL; BC017962; AAH17962.1; -.
Genew; HGNC:11067; SLC7A9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kidney Int. 59:1821-1833(2001).
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                                                                   "Non-type I cystinuria caus
subunit (b0,+AT) of rBAT.";
                                                                                                  Nat. Genet. 23:52-57(1999).
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346 CTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGA 405
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186 valileValalaileileileserGlyLeuValLeuLeuAlaGlnGlyAsnThrLys 205
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                                                                                                                                            /FTId=VAR_010260.
V->M: LOSS OF AMINO ACID TRANSPORT
                                                                                                                                                                                P -> S (IN REF. 2).
EF2C30DDE15594F1 CRC64;
                                     G -> R (IN CSNU3).
/FTIG-VAR_010256.
V -> M (IN CSNU3).
/FTIG-VAR_010257.
A -> T (IN CSNU3).
/FTIG-VAR_010258.
G -> R (IN CSNU3).
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Mismatches:
                                                                                                                      /FTId=VAR_010259.
G -> R (IN CSNU3).
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Matches:
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246 ArgAsnProTyrArgAsnLeuProLeuAlallelleIleGlylleProLeuValThrAla 265
                                                                  1546 GCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATC---ACTCTG 1602
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chairoungdua A., Segawa H., Kim J.Y., Miyamoto K.-I., Haga H., Fukui Y., Mizoguchi K.-I., Ito H., Takeda E., Endou H., Kanai Y., "Identification of an amino acid transporter associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, SUBUNITS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JNN-2002 (Rel. 41, Last annotation update)
16-JNN-2002 (Rel. 41, Last annotation update)
16(0,+)-type amino acid transporter 1 (B(0,+)AT) (Glycoprotein-associated amino acid transporter b0,+AT1).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELULAR LOCATION: Integral membrane protein (Probable).
TISSUE SPECIFICITY: KIDNEY AND SMALL INTESTINE. IN THE KIDNEY
TISSUE SPECIFICITY: KIDNEY AND SMALL INTESTINE. IN THE KIDNEY
SIGNAL AND THE APICAL MEMBRANE OF THE PROXIMAL TUBULES
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
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                                               TRANSPORT OF CYSTINE AND NEUTRAL AND DIBASIC AMINO ACIDS (SYSTEM B(0,+)-LIKE ACTIVITY). THOUGHT TO BE RESPONSIBLE FOR THE HIGH-APFINITY REABSORPTION OF CYSTINE IN THE KIDNEY PROXIMAL TUBULE. SUBUNIT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACID
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cystinuria-related type II membrane glycoprotein.";
J. Biol. Chem. 274:28845-28848(1999).
-!- FUNCTION: INVOLVED IN THE HIGH-AFFINITY, SODIUM-INDEPENDENT
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Conservative:
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InterPro; IPR004841; Permease.
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66.52$
44.13$
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                                                                               766 AATAGCATGAGTGAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTC 825
706 ATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTA 765
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RA Rajan D.P., Huang W., Kekuda R., Conway S.J., Devoe L.D.,
RA Leibach F.H., Prasad P.D., Ganapathy V.;
Leibach F.H., Prasad P.D., Ganapathy V.;
RT "Differential influence of the heavy chains 4F2hc and rBAT on Substrate affainty of the heteromeric b0, + amino acid transporter.";
RT Substrate affainty of the EMBL/Genbank/DbBJ databases.
C. - FUNCTON: INVOLVED IN THE HIGH-AFFINITY, SODIUM-INDEPENDENT
C. - FUNCTON: INVOLVED IN THE HIGH-AFFINITY, SODIUM-INDEPENDENT
C. - SUBCILIAR AND NEGTRAL AND DIBASIC ANINO ACIDS (SYSTEM CAFINITY REABSORPTION OF CYSTINE IN THE KIDNEY PROVIEM FHE HIGH-
C. - SUBCILLULAR LOCATION: INTEGRAL MEMBER WITH THE AMINO ACID
C. - SUBCELLULAR LOCATION: Integral membrane protein (Probable).
C. - SIMILIAR STRY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
FERNEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAAT)
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                                                                                                                                                                                                         STRAIN-FVB/N, and C57BL/6J;
MEDLINE-20056095; PubMed-10588648;
Pfeiffer R., Loffing J., Rossier G., Bauch C., Meier C., Eggermann T.,
Loffing-Cueni D., Kuehn L.C., Verrey F.;
"Luminal heterodimeric amino acid transporter defective in
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
B(0,+)-type amino acid transporter 1 (B(0,+)AT) (Glycoprotein-associated amino acid transporter b0,+AT1).
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InterPro; IPR004841; Permease.
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Transport; Amino-acid transport,
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                                                                                                          Mus musculus (Mouse).
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Length:
         3.16e-76
1067.50
66.30%
43.91%
25.91%
Alignment Scores:
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202 103 152

Conservative: Mismatches:

Best Local Similarity: Percent Similarity:

Query Match:

Indels:

Matches:

US-09-667-170A-440 (1-2239) x BAT1_MOUSE (1-487)

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346 CIGAAGAAGGAAAGICACTITACIGAGGGGAGICICCAIIAICATIGGCACCAICATIGGA 405
                                                                        406 GCAGGAATCTTCATCTCCTAAAGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCT 465
                                                                                                                                               CTGACCATCTGGACGGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAA 525
                                                                                                                                                                                                                     526 TIGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGT 585
                                                                                                                                                                                                                                                   86 LeuGlyThrMetIleThrLysSerGlyGluTyrProTyrLeuMetGluAlaPheGly 105
                                                                                                                                                                                                                                                                                            586 CCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACT 645
                                                                                                                                                                                                                                                                                                                    ||||:::|||||||:::::
|106 ProlleProAlaTyrLeuPheSerTrpThrSerLeuIleValMetLysProSerSerPhe 125
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                                                                                                                                                                                                                                                                                                                                                                     646 GCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAACCATTTTTATTCAATGTGAA 705
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| 126 AlaileileCysLeuSerPheSerGluTyrValCysAlaAlaPheTyrSerGlyCysLys 145
                                                                                                                                                                                                                                                                                                                                                                                                                                           706 ATCCCTGAACTIGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTA 765
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                     146 ProProAlavalvalValLysLeuLeuAlaAlaAlaAlaIleLeuPhelleThrThrVal 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    766 AATAGCATGAGTGTCAGCTGGAGGGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGGTC 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 AsnAlaLeuSerValArgLeuGlySerTyrValGlnAsnValPheThrAlaAlaLysMet 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           826 ACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAG 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                886 AACTITAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 AsnPheGlnAsnSerPheGluGlyThrGlnThrSerValGlyAlaIleSerLeuAlaPhe 225
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                                                                                              226 TyrAsnGlyLeuTrpAlaTyrAspGlyTrpAsnGlnLeuAsnTyrIleThrGluGluLeu 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 ArgAsnProTyrArgAsnLeuProMetAlaileVallieGlyIleProLeuValThrVal 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1366 CTCTTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTT 1425
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phis SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               1663 ATAATGTCAGAGAAAATAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAA 1722
                                                                                                                                                                                              1603 ACTGGAGTCCCTGCGTATTATCTCTTTATTATGGGACAAGAAACCCAGGTGGTTTAGA 1662
                                                                                                                               1546 GCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATC---ACTCTG 1602
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1426 ATTGGGCTGGCAGTTGCTGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGT 1485
                                                              1486 CCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTTCATGGTT 1545
                                                                                                                                                                                                                   464 ArgileSerArgProValThrLysHisLeuGlnMetLeuMetGluValValProProGlu 483
                                                                                  426 LeuAlaProlleIleSerGluProAlaTrpGluTyrLeuTyrCysValLeuPheIleLeu 445
                               386 TyrGlyMetThrIleLeuGlyLeuValValWatArgPheThrArgLysAspLeuGluArg 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isnard A.D., Thomas D., Surdin-Kerjan Y.; "The study of methionine uptake in Saccharomyces cerevisiae reveals new family of amino acid permeases."; J. Mol. Biol. 262:473-484(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HIGH AFFINITY PERMEASE FOR METHIONINE.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO YEAST LOW AFFINITY METHIONINE PERMEASE (MUP3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Entian K.D., Rose M., Koetter P., Roehmer A., Sehrsam I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport; Transmembrane. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
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IPR004760; L_AA_transport.
IPR004841; Permease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     High-affinity methionine permease.
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TIGRFAMS; TIGR00911; 2A0308; 1.
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141
183
208
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P50276:
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988 TITGTTACTGAAGAAGTAGAAAACCCTGAAAAACCATTCCCCTTGCAATATGTATATCC 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             766 AATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTC 825
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                                                                                                                                                                                                                                                                                                                                                                                                                         460 AIGICICIGACCAICTGGACGGIGIGIGGGGGTCCIGTCACIATITGGAGCTIIGICTIAI 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520 GCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTC 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 LeuAlaLeulleMetTrpAlaValGlyAlaIleIleAlaIleSerGlyLeuTyrValTyr 114
                                                                                                                                                                                                                                       280 GACGCCTTTTCAGGAAGACGCCTTTTCAGGAAGACGCCTTTTCAGGAAGAGAAAA 339
                                                                                                                                                                                                                                                                     36 AspAlaAspAsnGlyAlaSerAspPheGluAlaGlyGlnGlnPheAla---ThrGluLeu 54
                                                                                                                                                                                                                                                                                                                                55 AspGinGlyGluLysGlnLeuGlyIleLeuSerCysIleGlyLeuIleCysAsnArgMet 74
                                                                                                                                                                                                                                                                                                                                                                                 700 TGTGAAATCCCT-----GAACTTGCGATCAAGCTCATTACAGCT----
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                                                    F95D342814710837 CRC64;
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1135
1104
1199
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                                                                                                                                  Conservative:
Mismatches:
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                               POTENTIAL.
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361 PO
439 PC
476 PC
511 PC
63221 MW;
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                                                                                                                       368.50
45.61%
25.76%
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   341
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1108 GCTGAGGAGCTGCTTTCAAATGCAGTG---GCAGTGACCTTTTCTGAGGGGTACTG 1164
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                                                                                                                                                                                                    1222 AACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTT 1281
                                                                                                                                                                                                                                                                            1282 CCA------GAAAICCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTA 1326
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315 LysaspLysLeulleSerSerLysLeulleLeualaAlaAspPhePheAspIleValPhe 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1444 GGGCTGATTTATCTT------CGATACAAATGCCCAGATATGCATGGTCGTCCTTTC 1491
                                                                                                                                                              335 GlydlyglnAlaLysArgAlaAlaAlaAlaLeuValGlyLeuSerAlaLeuGlyAsnVal 354
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                                                                                                                                                                                                                                        355 LeuSerValllePheSerGlnGlyArglleIleGlnGlnLeuGlyArgGluGlyValLeu 374
                                                                                                                                                                                                                                                                                                                375 PropheSerAsnPhePheAla-SerSerLysProPheAsnSerProMetValGlyLeuPh 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 LeuLeuValGlnAsnLeuIleSerTyrProMetAsnIleIleAsnPheAlaIleSerAla 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1624 CTCTTTATTATATGGGACAAG---AAACCCAGGTGG-----TTTAGAATAATGTCAGAG 1674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 LysAlaGlyValPheValThrGlyPhePheThrLeuSerAsnLeuTyrLeuIleIleAla 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 ProTyrValProProSerAsnGlyGluSerValTyrSerSerMetProTyrTpIleHis 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 CysVallleAlaTrpGlyIlePhePhe------PheGlyGlyVal-----TyrTyr 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509 -----ValValTrpAlaGlnLeuLeuProArgTrpGlyHisTyrLysLeuValSerLys 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Saccharomyces
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01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                     "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 GCCTTTTCAGGAAGAGAG---AAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGA 375
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Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9C9767A181FDDCAE CRC64;
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Mismatches:
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Pro; IPR002293; AA/rel_prmeasel.
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MEDLINE=97049127; PubMed=8893857;
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. ≿		TCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATT 870	
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g	256	67.2	
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οy	1030	10	
Dp	294	313	
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g G		LeuPheThrLysLeuPheGlyProArgValGlyGlyLysPhe1lealaPhe 350	
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qq	351	370	
QY	1252	TTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGC 1311	
Db	371	387	
Οy	1312	AAGCACACTCCTCTACCAGCTGTTATGCTTTTGCACCCTTTGAATG 1359	
qq	388		
Qy	1360	ATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCTC 1404	
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                                                          1564 GACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATTAT 1623
                                                                                                                                                                          1624 CTC------ 1547
1465 AAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCC 1524
                   461 PheGlyValLeuAlaIleIleThrLeuSerLeuTyrMetLeuMetAlaProPheAla 480
                                                                                                                                              495 IleMetSerLeuLeuVallleValAlaCysPhePhePheTrpLeuValLysPheValLeu 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE=9742667; PubMed=9278503;
MEDLINE=9742667; PubMett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Escherichia.
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Hypothetical protein; Transport; Transmembrane;
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Science 277:1453-1474(1997).
                                                                                                                                                                                                                                    1648 ---CCCAGGTGGTTTAGAATA---ATGTCAGAGAAAATAACC 1683
                                                                                                                                                                                                                                                               515 LeuProLysPhePheHisTyrLysLeuLeuProLysIleThr 528
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
14-OCT-2001 (Rel. 40, Last annotation vigate)
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InterPro; IPR004841; Permease.
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EMBL; AE000413; AAC76395.1; ALT_INIT.
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			CATTGGCACCATCAT	yın	CGT(GTCI	GGAA	sAsr	CCCT	pAla	TATTCAATGT	AGTG	aPheMetLe	TTT		GGT		ACG Met/	AAC	: : eCysTy	TCCAT		Prop	CTG	(1eP	TTG 1
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276 LeuGlySerThrAlaGlyIlePheValAlaIleThrAlaMetIleValIleLeuGlySer 295
                                                                  316 PhePheLysCysPheGlyHisValHisProLysTyrAsnThrProAspValSerIlelle 335
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026594 schistosoma
Q9vy26 drosophila
Q9ty16 drosophila
Q9fs11 caenorhabdi
Q9hed neurospora
Q96083 caenorhabdi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim J.Y., Chairoungdua A., Cha S.H., Segawa H., Matsuo H., Kim D.K.,
Endou H., Kanai Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR004760; L_AA_transport.
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 Homo sapiens (Human)
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Q9BYH2
MODEL-frame+_n2P.model -DEV-x1h
-Q-(ggn2_1/USPTO_spool/US09667170/runat_04042003_090917_20296/app_query.fasta_1.2375
-DB-SPTREMBL21 -QFWT-fastan -SUFFIX-n2P.rspt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATIT-bloosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_NN-0 -ALIGN-15
-MODEL-LOCAL -OOTFMT--pc -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-USO9667170_eGGN_1 1_122_@funnat_04042001_20996 -NOFU-6 -ICPU-3
-NO_XLPXX -NO_MMAP -LARGEQUERY -NEC_SCORES-0 -WAIT -LONGLGG -DEV_ITIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                               (without alignments)
9561.440 Million cell updates/sec
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                                                                                                                                                                                       Description
                                                                                         April 16, 2003, 15:45:20 ; Search time 96.5 Seconds
GenCore version 5.1,3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                         OM nucleic - protein search, using frame_plus_n2p model
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1: Sp_archea:*
2: sp_bacteria:*
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4: sp_human:*
5: Sp_invertebrate:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                               424 CCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGCCATGTCTCTGACCATCTGGACGGTG 483
                                                                                                                                                            184 AAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGAGG 243
                                                                                                                                                                                                            244 CTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACGCC 303
                                                                                                                                                                                                                                                              304 TITICAGGAAGAGACGCCTITICAGGAAGAGAAAAGIGCAGCTGAAGAGGAAAGTCACT 363
                                                                                                                                                                                                                                                                           46 LeuLeuArgGlyValSerileIleIleIleGlyThrIleIleGlyAlaGlyIlePheileSer 65
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                                                                     118
                                                                        Conservative:
Mismatches:
                                                              Matches:
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                                                                                                                                     US-09-667-170A-440 (1-2239) x Q9BYH2 (1-494)
2A0308; 1.
            54423 MW;
                                                8.38e-205
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96.37%
96.37%
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TIGRFAMS; TIGR00911;
SEQUENCE 494 AA; 5
                                                                                         Best Local Similarity:
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1384 GACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTATTGGGCTGGCAGTTGCT 1443
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                                                                                                                                                                                                                                  1324 CTACCAGCIGITATIGITITGCACCCTITGACAAIGATAAIGCTCTTCTCTGGAGACCTC 1383
1144 ACCTITICIGAGCGGCTACIGGGAAATTICTCATIAGCAGTICCGAICTITGIIGCCCIC 1203
                                                                                                                  TCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTGCG 1263
                                                                                                                                                                          1264 ICICGAGAGGGICACCTICCAGAAATCCICCATGATICATGICCGCAAGCACACTCCI 1323
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIND=99449811: PubMed-10518579;
MEDIND=99449811: PubMed-10518579;
Medok R.J. Li J.Y., Nagaya M., Zhang C., Pardridge W.M.;
Selective expression of the large neutral amino acid transporter at the blood-brain barrier. The brood-brain barrier. Proc. Natl. Acad. Sci. U.S.A. 96:12079-12084(1999).
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                       SerCysPheGlySerMetAsnGlyGlyValPheAlaValSerArgLeuPheTyrValAla
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Blood-brain barrier large neutral amino acid transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOE6ECC11B8594E1 CRC64;
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Matches:
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InterPro; IPR004760; L_AA_transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00324; aa_permeases; 1.
TIGROMS; TIGRO0911; 2A0308; 1.
SEQUENCE 505 AA; 55110 MW; I
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<pre>illarity: 67.70% Conservative: 93 Similarity: 48.45% Mismatches: 153 indells: 3 6 Gaps: 1</pre>	70A-440 (1-2239) x Q9TU26	GCCTTTTCAGGAAGAGGCCCTTTTAGGAAGAGACGCCTTTTCAGGAAGAGAGAAGT 341 	CAGCTGAAGAAAGTCACTTTACTGAGGGGGGTCTCCATTATCAFTGGCACCATCAF 4 :: ::	AGCAGGAATCTTCATCTCTCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCAT 4 ::: :::::: :: VSerGLYIlePheValThrProThrGlvValIntrectural	TGACCATCTGGACGGGGTGTGGGGGTCCTGTCACTATTGGAGCTTTGTCTTATGC 5 LL ::	TGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTT 58	TCCATTACCAGCTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGCCTGCAGC 64.	GTGATATCCTGGCATTTGGACGCTACATTCTGGAACCATTTTTATTCAATG 70 :::::::	CCCTGAACTIGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGT 76 ::	TAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAA 82::	ACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAAC 88	GAACTITAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCC 93	GCCTTTTTATTATGGAATGTATGCATATGCTGGTTTTACCTCAACTTTGTAC 99 	AGTAGAAAACCGTGAAAAACCATTCCCCTTGCAATATGTATATCCATGCCAT 10 :::	GGTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAGG 11	SCTGCTTTCAATGCAGTGGCAGTGACCTTTTCTGAGCGG 	AGCAGTICCGATCTITGTIGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTT 12 :::	STCTCCAGGTATTCTATGTTGCGTCTCGAGAGGGTCAC
Similarity: al Similari tch:	-170A-440 (ccrrrrca gGlnAlaA	AGCTGAAG ::: hrLeuGln	TGGAGCAGG ::: eGlySerGl	GTCTCTGAC::::: uAlaLeuVa	TGAATTGGGAA aGluLeuGlyT	TGGTCCATTA:	TACTGCTGT : rGlnTyrIl	TGAAATCC ::: SProvalP	CCTAAATAGCAT ::: aValAsnCysTy	AG LA	< <	GGCTT uAlaL		₽ ⊐	CTGCTTTC LeuThrSe	GCAGTTCC ::: IleilePr	TCTC
Percent Best Loce Query Mai	99-60-	77 787 Dp 73	Oy 342 Db 42	Qy 402 Db 62	Qy 462 Db 82	Qy 522 Db 102	Oy 582 Db . 122	Oy 642 Db 142	Qy 702 Db 162	Oy 762 Db 182	Oy 822 Db 202	Qy 882 Db 222	Oy 936 Db 242	Qy 996 Db 262	Qy 1056 Db 282	Oy 1116 Db 302	Oy 1176 Db 322	Oy 1236

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1296 CATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGAC 1355
                                                                                  1356 AATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTGAATTTCCTCAGTTTTGCCAG 1415
                                                                                                                                          1416 GTGGCTTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCAGA 1475
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342 eThrSerSerArgLeuPhePheValGlyAlaArgGluGlyHisLeuProSerIleLeuSe 362
                                             442 uPheLeulleAlaValSerPheTrpLysThrProValGluCysGlyIleGlyPheThrIl 462
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-99047611; PubMed-9829974; MIDLINE-99047611; PubMed-9829974; Torrents D., Estevez R., Pineda M., Fernandez E., Lloberas J., Shi Y.B., Zorzano A., Palacin M.; Identification and characterization of a membrane protein (y+L amino acid transporter 1) that associates with 4F2hc to encode the amino acid transport activity y+L. A candidate gene for lysinuric protein
                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EA0E9782B3313B82 CRC64;
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230
94
149
18
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Mismatches:
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Matches:
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EMBL; AF019906; AAB93541.1; -
InterPro; IPR002293; AA/rel_prmeasel.
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InterPro; IPR004841; Permease.
Pfam. PF00324; aa_permeases; 1.
TIGREAMS; IIGR00911; 280308; 1.
SEQUENCE 507 AA; 55595 MW; EA0E9
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1270 GAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCA 1329
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US-09-667-170A-440 (1-2239) x 057439 (1-507)
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Mastroberardino L., Spindler B., Pfeiffer R., Skelly P.J., Loffing J., Shoemaker C.B., Spindler B., Pfeiffer R., Skelly P.J., Loffing J., Shoemaker C.B., Phidler B., Pfeiffer R., Skelly P.J., Loffing J., Shoemaker C.B., Phidler B., Ph
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                                                                                                                                                                                                                                                                                                                                                          1450 AITTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATC 1509
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1330 GCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTCTTGGAGACCTCGACAGT 1389
                                                                                                                                                                        1390 CITTIGAATTICCICAGITTIGCCAGGIGGCTTTITATIGGGCTGGCAGTIGCTGGGCTG 1449
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                                                                                                                                                                                                                                                             396 ValileAsnPhePheSerPhePheAsnTrpLeuCysValAlalaLeuAlaIleIleGlyMet 415
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Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97324256; PubMed-9178633;
Spindler B., Mastroberardino L., Custer M., Verrey F.;
"Characterization of early aldosterone-induced RNAs in A6 kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G -> A (IN REF. 0).

A -> R (IN REF. 0).

F -> L (IN REF. 0).

N -> D (IN REF. 0).

M, 2A6741CE89AB721D CRC64;
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MEDLINE=98421678; PubMed=9751058;
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391 391 N
507 AA; 55529 MW;
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Alignment Scores:

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507 229 94 150 18		CTTT	GACGCCTTTTCAGGAAGAGAGAAGTGCAGCTGAAGAGAAAGTCACTTTACTG	: : eThrLeuV	CTCCATTATCATIGGCACCATCATIGGAGCAGGAATCTTCATCICTCCTAAGGGGG ::: :::	TCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGG ::::	CTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGT 	CATTACACATATATTTTGGAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGT 	GTGATATCCTGGCATTTGGACG	ATTCTGGAACCATTTTTTTTTGTGTGAAATCCCTGAACTTGCGATCAAGCTCA :::	GTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGG :::	CTTAACCTTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGG 	GCCTJ ::: UArgSerP	AGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTATGCATAT 	GGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCTGAAAAAACCATTCCC 	GCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAATGTGGCC 	TACTTTACGACCATTAATGCTGAGAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTT 	STTGCCCT alglyLe
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Length: Matches: Conservati Mismatches Indels:	507)	CTTTTCAG ::: YGlyAla	GCTGAAG	urenglu	AGCAGGA ::: ySerGly]	TCTGACCA rLeuLeuV	ATTGGGAA uLeuGlyT	TCCATTAC	rgcrgrgA :::: TyrIlev	AATCCCTG ::: : oValProA	AAATAGCA ASnCysT	ACAGCAA' : LeuAlaL	TGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGAC :: alGlnLeuGlyLySGlyGlyValGluAspLeuLySPro	GCTTTT7	GAAGTAGA ::: GluMetI]	ACCATTGG ::: ThrLeuVa	CTGCTTTC LeuAsnSe	TCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGC GlyAsnTyrHisLeuGlyValMetAlaTrpIleIleFroValPheValGl
m	13020 (1	CAGGACGC 31yAspG1	AAAGTGCA	valgl	ATCATTGG leileGl	GCATGTC ::: YLeuSe	ATGCTGA	TCTTTGG	CAGCTAC	AATGTGA hrCysPro	TGGTCCTA ::: hrAlaile	GCAAGCTC aLysLeu	AAACGCAG ::: lyvalglu	rGCCACTG rpValLeu	FTACTGAA ValGlu	CCATTGTC 	GGAGCTG :::::: uGlnMet	CTCATTA(::: tAlaTrp
4.09e-91 1213.00 65.78% 46.64% 29.44%	239) x 0	GGCAACAAGGAGCCACCTGGGCAGGACGC 	AAGAGAG		TGGCACC	CAGCGTGC ySerProC	TTTGTCTT aLeuCys1	TTTGGAAG	GAACTCCTCATAATACGCCCTGCAGCTACTGCT 	TTTATTC PheProT	rGTAGTGA :::::: LeuLeuT	AACCTTTT BAlaAlaA	TAAAGGTC LysGlyG	ACGCGGT:	AACTTTG: 	TCCATGGG	AATGCTGA ThrProG]	GGAAATT1 GlyValMe
.ty: .arity:	40 (1-2	AAGGAGCC AlaGluPr	TTTTCAGG		ATTATCAT :: IleIleVa	AACACGGG 31uAlaGl	TCACTATTGGAGCTTTGTC ::: SerlleValGlyAlaLeuCy	ACATATAT ::	TCATAAT 	SAACCATT ::[1] ysProva	GCATAAC	CAGATTTTCTT/ GlnAspalaPhe	AGCTAAT7 nLeuGly	CAAGTATT :::::::: hrAsnVal	TTACCTC snTyrLeu	TATGTATA	CGACCATT ::: hrThrLeu	GCTACTG rHisLeu
No.: : nt Similarity: Local Similari Match:	7-170A-4	6 GGCAAC 		;	Va – GT	P = 3	E 0			ATTCTGG ::: : LeuLeuI	GCTGTGG ::: CysLeuC	ATCCAGATT ::: ValGlnAsp	GTTATGC ::: PhevalG	AGAGATT : ThrSerT	GGCTGGT GlyTrpA	CTTGCAAT Argalail	TACTTTAC TyrPheT	TCTGAGCC GlyAsnTy
Pred. No.: Score: Percent Sim Best Local Query Match DB:	99-60-	33.	31	4	376	436	496	556	616	676 156	736	796	856 216	910	970	1030	1090	316
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1210 TTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTGCGGTTCGA 1269
                                                                 1270 GAGGGTCACCTTCCAGAAATCCTCCCATGATTCATGTCCGCAAGCACACTCCTCTACCA 1329
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                   376 SerLeullepheThrCysAlaMetThrLeuLeuTyrAlaPheSerAsnAspIlePheSer 395
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
50lute carrier family 7 (cationic amino acid transporter, y+ system),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 GACGCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAAAA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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31 GlualaargargGlyaspGlyalaaspProGluGlyGluGlyValThrLeuGlnargasn
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026131; AAH26131.1; -.
SEQUENCE 512 AA; 55872 MW; 57045EC4DD9DE1AI CRC64;
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TISSUE=SALIVARY GLAND;
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1300 ATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATG 1359
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                                                                                                                                                                                                                                                                                                          151 LeuValPheAlaThrTyrLeuLeuLysProValPheProThrCysProValProGluGlu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                    718 GCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGGTGGTCCTAAATAGCATGAGT 777
                                                                                                                                            538 ATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGTCCATTACCAGCT 597
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                                                                                                                      478 ACGGIGIGIGGGGICCTGICACIATIIGGAGCIIITGICTIAIGCIGAAIIGGGAACAACI 537
                                       418 ATCTCTCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGG 477
51 IleThrLeuLeuAsnGlyValAlaIleIleValGlyThrIleIleGlySerGlyIlePhe 70\,
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247 CCITCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTITTCAGGAAGAGAGACGCCTIT 306
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                                                                                                                                           1600 CIGACIGGAGICCCIGCGIAIIAICICITIAIIAIAIGGGACAAGAAACCCAGGIGGIII 1659
                                                                                                                                                                                                                1660 AGAATAATGTCAGAGAAAATAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAA 1719
1480 CATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTC 1539
                                                                      1540 ATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACT 1599
                                                                                                       451 LeulleAlaValSerPheTrpLySThrProMetGluCysGlyIleGlyPheAlaileile 470
                                                                                                                                                                                                                                     471 LeuSerGlyLeuProValTyrPhePheGlyValTrpTrpLysAsnLysProLysTrpIle 490
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SEQUENCE FROM N.A.
A Miyamoto K., Endou H., Tani Y., Ohkido M., Segawa H., Kanai Y.,
A Miyamoto K., Endou H., Takeda E.;
Miyamoto K., Endou H., Takeda E.;
Miyamoto K., Endou H., Takeda E.;
Miyamoto F. the human sodium-independent neutral amino acid
RT "Induction of the human sodium-independent neutral amino acid
RT submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
BERL, AB023712; BAB70708.1; JOINED.
BERL, AB023714; BAB70708.1; JOINED.
BERL, AB023715; BAB70708.1; JOINED.
BERL, AB023716; BAB70708.1; JOINED.
BERL, AB023717; BAB70708.1; JOINED.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sodium-independent neutral amino acid transporter LAFI.
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TIGRFAMS; TIGR00911; 2A0308; 1
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961 GCATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAA 1020
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                                                367 CTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCTCCT 426
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34 GlyAlaAlaProAlaGlyGluGly---GluGlyValThrLeuGlnArgAsnIleThrLeu 52
                                                                                  53 LeuAsnGlyValAlaIleIleValGlyAlaIleIleGlySerGlyIlePheValThrPro 72
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1441 GCTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCA 1500
                                                                                                             1501 CIGITCAICCCAGCIITGIITICCIICACAIGCCICITCAIGGIIGCCCIIICCCICIAI 1560
                                                                                                                                                                                       1561 TCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTAT 1620
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Torrents D., Estevez R., Pineda M., Fernandez E., LLoberas J.,
Shi Y. Eb., Zorzano A., Palacin M.;
Identification and characterization of a membrane protein (y+LAT-1)
that associates with 4F2hc to encode the amino acid transport activity
y+L. A candidate gene for Lysinuric protein intolerance.";
J. Biol. Chem. 273:32437-32445(1998).
EMBL: D87432; BAA13376.1;
InterPro; IPR002293; AA/rel_prmeasel.
                                                                                                                                                                                                                                                                 1621 TATCTCTTTATTATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAATA 1680
393 IlePheSerValIleAsnPhePheSerPhePheAsnTrpLeuCysValAlaLeuAlaIle 412
                                                               413 IleGlyMet1leTrpLeuargHisArgLysProGluLeuGluArgProIleLysValAsn 432
                                                                                                                                                 433 LeuAlaLeuProValPhePheIleLeuAlaCysLeuPheLeuIleAlaValSerPheTrp 452
                                                                                                                                                                                                                 453 LysThrProValGluCysGlyIleGlyPheThrIleIleLeuSerGlyLeuProValTyr 472
                                                                                                                                                                                                                                                                                                     473 PhePheGlyValTrpTrpLysAsnLysProLysTrpLeuLeuGlnGlyIlePheSerThr 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; Prediction of the coding sequences of unidentified human genes. VI. the coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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141
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Last annotation update)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE-97191544; Pubmed-9039502;
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SEQUENCE 515 AA; 56827 MW;
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69.16%
46.68%
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                                        394 ACCATCATTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGCTCCAGAACACGGGCAGC 453
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                                                            37 GluThrMetGlnLeuLysLysGluIleSerLeuLeuAsnGlyValSerLeuValValGly 56
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                                                                            STRAIN-NIH/SWISS; TISSUE-HEART;
MEDLINE-99094891; PubMed-9978049;
Pfeiffer R., Rossier G., Spindler B., Meier C., Kuhn L., Verrey F.;
Manino acid transport of y-L-type by heterodimers of 4F2hc/CD98 and
members of the glycoprotein-associated amino acid transporter
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last Sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Mismatches:
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InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004841; Permease.
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Pfam; PF00324; aa_permeases; 1
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              1234 TITGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
514 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 573
                                                        574 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGC 633
                                                                           694 ATTCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 753
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                                                                                                                                                                                                                                                                                                                  230 AlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSerGlyTrpAspThrLeuAsnTyrVal 249
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                                                                                                                  CCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAACCATTTTTT
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1645 AAACCCAGGTGGTTTAGAATAATGTCAGAGAAATAACCAGAACATTACAAATAATA--- 1701
469 ArgProLeuPheLeuArgArgIleValAlaSerIleThrArgTyrLeuGlnIleLeuCys 488
                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Y+LAT1a (Solute carrier family 7 (Cationic amino acid transporter, y+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 GAGAAAAGTGCAGCTGAAGAAGAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 ACCATCATTGGAGCAGGAATCTTCATCTCCTAAGGGCGTGCTCCAGAACACGGGCAGC 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99094891; PubMed=9878049; Pfeiffer R., Rossier G., Spindler B., Meier C., Kuhn L., Verrey F.; "Amino acid transport of y+L-type by heterodimers of 4F2hc/CD98 and members of the glycoprotein-associated amino acid transporter
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9F30FB1B88126F6C CRC64;
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InterPro; IPR004841; Permease.
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                                                                                                    1702 CTGGAAGTTGTACCAGAAGAT 1725
                                                                                                                                489 MetServalAlaAlaGluMetAsp 496
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1354 ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTGAATTTCCTCAGTTTTGCC 1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1594 AICACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTATA------TGGGACAAG 1644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1474 GATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGC 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1234 TTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               994 ACTGAAGAAGTAGAAAACCCTGAAAAACCATTCCCCTTGCAATATGTATATCCATGGCC 1053
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                                                                                                                                                                                                                                                                                                                   874 GGTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG 933
                                                                                                                                                                                                                                                                                                                                                                                      150 ProSerCysGlyAlaProTyrAlaAlaGlyArgLeuLeuAlaAlaAlaAlaCysIleCysLeu 169
                                                                                                                                                                                                                                                        170 LeuThrPheIleAsnCysAlaTyrValLysTrpGlyThrLeuValGlnAspIlePheThr 189
                   694 ATTCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 753
574 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 AlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSerGlyTrpAspThrLeuAsnTyrVal
                                                                      634 CCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAACCATTTTTT
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670 CGCTACATICIGGAACCATITITIATICAATGIGAAAICCCIGAACTIGCGAICAAGCIC 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730 ATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGC 789
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                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::||| ::: ||| ::: ||| 469 ArgProLeuPheLeuArgArgIleValAlaSerIleThrArgTyrLeuGlnIleLeuCys 488
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                                                                                                                                                                                                                                                                                                                                                            Kanai Y., Fukasawa Y., Segawa H., Endou H.; "Characterization of a system y+L amino acid transporter."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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217
103
152
                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Mismatches:
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Matches:
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Interpro; IPR002293; AA/rel_prmeasel.
Interpro; IPR004841; Permease.
                                                                                                                                            PRT;
                                               1702 CTGGAAGTTGTACCAGAAGAAGAT 1725
                                                                              489 MetSerValAlaAlaGluMetAsp 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00324; aa_permeases; 1. SEQUENCE 512 AA; 55641 MW;
                                                                                                                                                                                                                      Y+L amino acid transporter 1. RY+LAT1.
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1131.50
67.378
45.688
27.468
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                      TISSUE=KIDNEY;
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                                                                                                                                                                                                          01-MAR-2002
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970 GGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAAACCATTCCC 1029
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790 GCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATAATTATAGTC 849
                       850 CCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGA 909
                                                                                          910 AGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTATGCATATGCT 969
                                                                                                                                                                 224 SerSerPheAlaMetGlyAspIleAlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSer 243
                                                                                                                                                                                                                     1510 CCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCA 1569
                                                                                                                                                                                                                                                                                                                                                                   284 TyrTyrSerValLeuAspIleLysAspIleLeuAlaSerAspAlaValAlaValThrPhe 303
                                                                                                                                                                                                                                                                                                                                                                                                                        304 AlaAspGlnIlePheGlyIlePheAsnTrpThrIleProLeuAlaValAlaLeuSerCys 323
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             310 GGAAGAGACGCCTTTTCAGGAAGAGAAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTG 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 GlyAspGlyAlaGlyProAlaAlaGluGlnValLysLeuLysLysGluIleSerLeuLeu 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ng A.M.L., Yao S.Y.M., Cheeseman C.I., Young J.D., "CDNA encoding rat jejunal amino acid transporter y+LATI."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                    Pfam; PF00324; aa_permeases; 1.
SEQUENCE 512 AA; 55684 MW; 708905B2ACB2130B CRC64;
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217
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Indels:
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Matches:
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                                                                                                                                                                 EMBL, AF200684; AAF07216.1; InterPro; IPR002293; AA/rel_prmeasel. InterPro; IPR004841; Permease.
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1131.50
67.37%
45.68%
27.46%
                                                                                                    STRAIN-SPRAGUE-DAWLEY;
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                                                                                   SEQUENCE FROM N.A
                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                       Alignment Scores:
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1630 ATT-----ATAIGGGACAAAGAACCCAGGIGGIIIAGAAIAAIGICAGAGAAAAIAACC 1683
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                                                                          1090 TACTITACGACCATTAATGCTGAGGAGCTGCTGTTTCAAATGCAGTGGCAGTGACCTTT 1149
                                                                                                                                                     1150 TCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGC 1209
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1030 CITGCAATAIGTATACCATGGCCATTGTCACCATTGGCTATGTGCTGACAAATGTGGCC 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20196065, PubMed-10731132;

MEDLINE-20196066; PubMed-10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                   324 PheGlyGlyLeuAsnAlaSerIleValAlaAlaSerArgLeuLeuPheValGlySerArg 343
                                                                                                  1684 AGAACATTACAAATAATA---CTGGAAGTTGTACCAGAAGAAGAT 1725
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAX-2002 (TrEMBLrel. 20, Last annotation update)
CG1607 protein (Fragment).
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshavov S., RA Borkova D. Botchan M.R., Bulck J., Brokstein P., Blotchan M.R., Bulck J., Brokstein P., Blotchan M.R., Bulck J., Brokstein P., Brotlier P., Burtis K.C., Busam D.A., Baller H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Deng Z., Mays A.D., David I., Davids P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dowe I., Dietz S.M., RA despisata C.C., Ferraz C., Ferriera S., Fleischmann W., RA Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Hartis N.L., Harvey D., Heinan T.J., Hernandez J.R., Hartis M., Alalai M., Kalush F., Gong F., Gorrell J.H., Gu Z., Genbart W.M., Glasser K., RA Hostin D., Houston K.A., Howland T.J., Herning D. J., Ling Y., Lin X., Mattel B.E., Kodira C.D., Kraft C., Liz J., Ling Y., Lin X., RA Lasko P., Lei Y., Lei Y., Li Z., Ling Y., Lin X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Lasko P., Lei Y., Mutrib U., Muzny D.M., Nollson D.L., RA Melson D.R., Nelson K., Nishina N.V., Mobarry C., Morris J., Noshrefi A., Shue B.C., Stenellar R., Shen H., Wang X., Ranger B.C., Stenellar R., Verlame S., Pollard J., Puri V., Ressem C., Stapler E., Shen H., Wang X., RA Sylrskas R., Tector C., Turner R., Vang S., Vao Q., Rangen B.C., Stanen C., Staplecon M., Stupski M.P., Shith H.O., RA Yelliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Zhen R., Welssenbach J. S., Rangence C., Broadling A.C., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Shith H.O., RA Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu Zhu S
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Mismatches:
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Interpro; IPR002422; AA/rel_prmease2.
Interpro; IPR004841; Permease.
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FlyBase; FBgn0039844; CG1607.
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1675 AAAATAACCAGAACATTACAAATAATACTGGAAGTTGTA 1713

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955 ATGTATGCATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCT 1014
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108 MetileThiLysSerGlyAlaAspTyrAlaTyrIleMetGluThrPheGlyProPheMet 127
                                 595 GCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATA 654
                                                      655 TCCCIGGCATITGGACGCIACAITCIGGAACCAITITITIAITCAATGIGAAAICCCIGAA 714
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                                                                                                                             715 CITGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATG 774
                                                                                                                                                                                                              168 AspSerAlaArgLeuLeuAlaValCysCysIleLeuValLeuThrLeuIleAsnCysTrp 187
                                                                                                                                                                                                                                                775 AGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATT 834
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                                                                                                                                                                                                                                                                                                                       835 CTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAA 894
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R. Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Barandon R.C., Rogers Y. H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
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R. Buttis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
R. Buttis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
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R. Dockon K., Doup L.E., Downes M., Down I., Dev I., Dietz S.M.,
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R. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris N.L.,
R. Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
R. Alasko P., Lei Y., Leyther G. H., Karpen G. H., Karvitz S., Kullp D., Lai Z.,
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R. Shier E., Spradling A.C., Strepleton M., Stupski M.P., Saith T.,
R. Syler R., Stradling A.C., Strapleton M., Stupski M.P., Wang S., Pan S.,
R. Syler R., Shill R., Wang Sarman D.A., Wang S., Pan S
                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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"The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Minidiscs encodes a component of an endocrine signaling pathway required for normal imaginal cell proliferation."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                               Last sequence update)
Last annotation update)
486 GlyLeuThrGlnValLeuGlnLysLeuMetMetValVal 498
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                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequ
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                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                        MND protein (LD25378p).
MND OR CG3297.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                       01-NOV-1999
01-MAR-2002
                                                                                                                  Q9Y1A7
                                                                  RESULT 13
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985 AACITIGITACIGAAGAAGTAGAAAACCCIGAAAAACCAITCCCCTIGCAAIAIGIATA 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 LeuPheAspGlyAsnThrGluHisTrpAspAsnProPheSerGlyGlyLeuGlnAspPro 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 ileCysValLeuThrLeuIleAsnCysTyrAsnValLysTrpValThrArgValThrAsp 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 ileLeuValProThrGlyAsnAlaIleThrAlaLeuThrPheAlaIleTyrLeuLeuLys 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      685 · CCATTTTTATTCAATGIGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGC 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       805 ITCITAACCITITGCAAGCICACAGCAATICIGATAATIATAGICCCIGGAGTIAIGCAG 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATATITIGGAAGICTITIGGICCATIACCAGCTITIGIACGAGICTGGGIGGAACICCIC 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 ATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAA 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 GGAGCTITGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                  325 TCAGGAAGAGAGAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 ATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCTCCTAAGGĠCGTGCTCCAGAAC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 ACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGGTCCTGTCACTATTT 504
                                                                                                                                                                                                                                                                                                                                                                  265 GAGCCACCTGGGCAGGACGCCTTTTCAGGAAGACGCCTTTTCAGGAAGAGACGCCTTT 324
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72 SerGlySerIleGlyGlnSerLeuIleValTrpValLeuSerGlyValLeuSerMetVal 91
                                                                                                                                                                                                                                                                                                                                                                                                   22 GluproAsnAsnSerThrAlaAspSerGlySerGlnGly------34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 SerGly------ValLysLeuLysLysGlnIleGlyLeuLeuAspGlyValAlaile 51
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003532; AAR49688.1; -
                                                                                                                                                                        E2882CC0737CC56F CRC64;
                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
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                                                                                                      Flyase: FBG0002778; mnd.
Interpro; IPR002293; AA/rel_prmeasel.
Interpro; IPR004841; Permease.
                                                                                                                                                           Pfam; PF00324; aa_permeases; 1.
SEOUENCE 499 AA; 54350 MW;
                                                                          AF139834; AAD39459.1; -.
                                                                                        EMBL; AY069533; AAL39678.1; -.
                                                                                                                                                                                                                        1.09e-88
1106.00
65.57%
44.67%
26.84%
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Best Local Similarity:
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1585 GGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTTATTATATGGGACAAG 1644
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                                                                                                                                                                                                                                                                                                                                                                                     1405 AGITITGCCAGGTGGCITTITATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATAC 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1525 IICACATGCCICTICAIGGIIGCCCTITCCCICIAITCGGACCCAITIAGIACAGGGAIT 1584
                                                                                                                                                                                                                                                                                                                        1345 CACCCTTTGACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCTC 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1465 AAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCC 1524
1045 ICCAIGGCCAITGICACCAITGGCTAIGIGCIGACAAAIGIGGCCIACIITACGACCAII 1104
                                                                                                                                                                                             1225 GGIGGIGITITGCIGICTCCCAGGITAITCIAIGTIGCGICTCGAGAGGGICACCTICCA 1284
                                                                                                                                                                                                                                                          1285 GAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTG 1344
                                                                                                                                                                                                                                                                                                                                                                                                          470 ProvalLysTrpLeuAlaAspThrSerGlnAlaileAsnLeuTrpCysSerLysPhePhe 489
                                                                1105 AATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTG 1164
                                                                                                                              1165 GGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAAC 1224
                                                                                                                                                                                                                                                                               312 GlyTyrMetSerTrpIleMetProPheAlaValAlaCysSerThrPheGlySerLeuAsn 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rajan D.P., Kekuda R., Huang W., Devoe L.D., Leibach F.H., Prasad P.D., Ganapathy V.; "Cloning and functional characterization of a Na(+)-independent, broad-specific neutral amino acid transporter from mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL, AF170106; AAF26282.1; -
InterPro; IPR002293; AA/rel_prmeasel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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961 GCATATGCTGGCTGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAA 1020
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                                                                                                                                                                                                                                                              316 GACGCCTTTTCAGGAAGAGAGAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGA 375
                                                                                                                                                                                                                                                                                                                                        435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 ThralavalGlyAlaLeuCysTyrAlaGluLeuGlyValThrIleProLysSerGlyGly 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 AlaValLeuVallleTyrProThrAsnGlnAlaVallleAlaLeuThrPheSerAsnTyr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           676 ATTCTGGAACCATTTTTATTCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACA 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 ValGlnAspIlePheThrAlaGlyLySLeuLeuAlaLeuAlaLeuIleIleIleMetGly 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTATGCAGCTAATTAAAGGT------CAAACGCAGAACTTTAAAGACGC 900
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                                                                                                                                                                                                                                                                                                                                                46 CysGlyIleIleValGlyAsnileIleGlySerGlyIlePheValSerProLysGlyVal 65
                                                                                                                                                                                                                                                                                               26 GluAlaSerSerGlyGlyGlyValAlaLeuLysLysGluIleGlyLeuValSerAla
                                                                                                                                                                                                                                                                                                                             376 GTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                           66 LeuGluAsnAlaGlySerValGlyLeuAlaValIleValTrpIleValThrGlyLeuIle
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Mismatches:
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InterPro; IPRO04760; L_AA_transport.
InterPro; IPRO04841; Permease.
Pfam, PF00324; aa_permeases; 1.
TIGRFAMS; TIGR00911; 2A0308; 1.
SEQUENCE 535 AA; 58321 MW; D4939
                                                                                                                  1.03e-87
1095.00
65.97%
45.38%
26.58%
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Best Local Similarity:
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DB:
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RX MEDILINE-20196006; pubmed=10731132;
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Mogers Y.-H.C., Blazej K.G., Champe M., Pfeilfer B.D.,
RA Mank M., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Butris K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                1201 CTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCCAGGTTATTCTATGTT 1260
                                                                                                                                                             1261 GCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACAT 1320
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                                                                                                          324 LeuSerThrPheGlyGlyValAsnGlySerLeuPheThrSerSerArgLeuPhePheAla 343
                                                                                                                                                                                         344 GlyAlaArgGluGlyHisLeuProSerValLeuAlaMet1leHisValLysArgCysThr 363
                                                                                                                                                                                                                                                                                    384 MetTyrThrLeuIleAsnTyrValGlyPheIleAsnTyrLeuPheTyrGlyValThrVal 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 SerGluProValValCysGlyIleGlyLeuAlaIleMetLeuThrGlyValProValTyr 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 PheLeuGlyValTyrTrpGlnHisLysProLysCysPheAsnAspPhelleGluLeuLeu 483
                   ValThrPheGlyGluLysLeuLeuGlyValMetAlaTrpIleMetProIleSerValAla 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 AlaGlyGlnIleValLeuArgTrpLysLysProAspIleProArgProIleLysIleAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 LeuLeuPheProIleIleTyrLeuLeuPheTrpAlaPheLeuLeuIlePheSerLeuTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1681 ACCAGAACATTACAAATAATACTGGAAGTTGTA---CCAGAAGAAGAT 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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protein (GH08870P).
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RA Harris. N.L., Howland T.J., Wei M.H., Degwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
R. Jasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lidng Y., Lin X.,
R. Liu X., Mattel B., McIntosh T.C., Morris J., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Pacleb J.M.,
RA Melson D.K., Nelson K., Nixon K., Nisskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Standling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Weinsteck G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Weinsteck G.M., Weissenbach J.,
RA Te J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RA Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.;
RA The genome sequence of Drosophila melanogaster.";
R. Science 287:2185-2195(2000).
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                                                                                    652 ATATCCCTGGCATTTGGACGCTACATTCTGGAACCATTTTT----ATTCAATGTGAAATC 708
                                                                                                                               157 MetGlyLeuThrPheAlaSerTyrValLeuGluProPhePheGlyGlyAlaCysGluIle 176
                                                                                                                                                                                                               177 ProLysIleAlaLeuGlnLeuLeuAlaAlaIleThrIleCysPheLeuThrTyrLeuAsn 196
                                                                                                                                                                                                                                                             769 AGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACA 828
                                                                                                                                                                                                                                                                                                                                                  829 GCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAAC 888
                                         137 ProAlaPheLeuTyrLeuTrpAspAlaMetMetilePheValProThrThrAsnAlalle 156
                                                                                                                                                                           CCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAAT 768
592 CCAGCITITIGIACGAGICIGGGIGGAACTCCICATAAIACGCCCTGCAGCIACIGCIGIG 651
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Gapop 60.0 , Gapext 60.0
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1-549-2 ce 2, Application US/08861549 No. 587446 AL INFORMATION: LICANT: Goli, Surya K. LICANT: Coli, Surya K. LICANT: Bandman, Olga LICANT: Bandman, Olga LICANT: Inspective Pharmaceuticals, Inc. PREED: 3174 Porter Drive RESPONDENCE ADDRESS: RESPONDENCE ADDRESS: RESPONDENCE BADRESSOR RESPONDENCE ADDRESS: RESPONDENCE BADRESSOR RESPONDENCE ADDRESSOR RESPONDENCE BADRESSOR RESPONDENCE BADRESSOR RESPONDENCE BADRESSOR RESPONDENCE BADRESSOR RENT RADALICATION DATA: RENT APPLICATION DATA: RENT APPLICATION DATA: LING DATE: RAPLICATION NUMBER: US/08/861,549 LING DATE: LING DATE: RENEWCAGEAT INFORMATION: LING DATE: RENEWCAGEAT NUMBER: 36,749 SELICATION NUMBER: 36,749 COMMUNICATION INFORMATION: LIEFAN: A15-845-456 RAIDENCE: LIE-845-456 RAIDENCE: LIE-845-416 RANDEDNESS: SINGle SEASON NOT SECONDESS: RANDEDNESS: SINGle RANDEDNESS: SINGle RANDEDNESS: SINGle SEASON NOT SECONDESS: RANDENCE: RANDEDNESS: SINGle SEASON NOT SECONDESS: RANDEDNESS: SINGle RANDENCE: RANDEDNESS: SINGle SEASON NOT SECONDESS: RANDEDNESS: SINGle RANDEDNESS: SINGle SEASON NOT SECONDESS: RANDEDN	Matches 27; Conservative 0; Mismatches 0; Indels

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OTHER INFORMATION: 5-135-198 ; polymorphic base insertion of GTTT
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INFORMATION: 5-145-24 : polymorphic
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OTHER INFORMATION: 5-140-361
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LOCATION: 72771..72817
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US-09-345-882-1/C
Sequence 1, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
CURRENT FILING DATE: 1999-06-30
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR APPLICATION DATE: 1998-12-10
PRIOR FILING DATE: 1998-12-10
                                                                                                        Sequence 18, Application US/09780049
Factor No. 6465250
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
TITLE OF INVENTION: EXPRESSION
FILE REPRENCE: RTS-0134
CURRENT APPLICATION NUMBER: US/09/780,049
CURRENT APPLICATION NUMBER: US/09/780,049
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 96
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SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 24; Conserv
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                                                                                             RESULT 2
US-09-780-049-18/c
                                                                                                                                                                                                                                                                                                                   ENGTH: 40000
                                                                                                                                                                                                                                                                                                                                                                                  US-09-780-049-18
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                                                                                                                                                                                                                                                                                                    SEQ ID NO 18
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                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
                                                                                                                                                                                                                               OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
                                                                                                                                                                                                                                                                                      LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME_KEY: allele
LOCATION: 97099. 97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KET: allele
LOCATION: 97099.,97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
                                                 LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
                                                                                                                                 LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele .
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
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                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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LOCATION: 106918..106966
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LOCATION: 103783..103828
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                                                                                                            NAME/KEY: allele
LOCATION: 88050..88096
                                                                                                                                                                                                                 90819..90865
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                                      NAME/KEY: allele
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                                                                                                                                                                                                LOCATION: 108127...108177
UCCATION: 108127...108177
FEATURE:
NAME/KEY: allele
LOCATION: 108127...108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
                                                                                                                       LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/nnn ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AxyS Pharmaceuticals, Inc.
TILE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 54003 CCAGCCTGGGTGACAGTGAGACTC 53980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650.327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 CCAGCCTGGGTGACAGTGAGACTC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09009913
Patent No. 6087485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2: CLASSIFICATION:
                                                                                                    NAME/KEY: allele
                                                                                                                                                              FEATURE:
NAME/KEY: allele
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TITLE OF INVENTION: Microsatellite Sequences for Canine TITLE OF INVENTION: Genotyping NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,906A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.0%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 4.5 Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PB1508USM CURRENT APPLICATION NUMBER: US/08/646,301A CURRENT FILING DATE: 1996-05-16 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                  A-62282/BIR
                                                                                                                                                                                                                                   COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: A 62
TELECOMMUNICATION INFORMATION:
TELEFAN: 415-781-1989
TELEFAX: 415-781-1989
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AAAAAAGAAAGAAAGA 142
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                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                          COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 110..195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 350 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                        STATE:
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APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
TITLE OF INVENTION: REPEAT DNA MARKERS
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            0; Indels
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MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
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                0; Mismatches
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OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97 (DOS text format)
CURRENT APPLICATION DATA:
FILING DATE: 04-Feb-1998
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                                                                     Db 47805 GAGGTTGAAGTGAGCAGAGATCA 47783
                                                                                                                                                                  US-09-018-584A-27; Sequence 27, Application US/09018584A; Patent No. 6238863
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Promega Corporation
STREET: 2800 Woods Hollow Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0°;
100.0%; Prr
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                                                  2 GAGGTTGAAGTGAGCAGAGATCA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 257-3501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHROMOSOME/SEGMENT: 15q26.2
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Dvorak, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (608) 257-2275
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halverson, Joy
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nes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Nucleic Acid
STRANDEDNESS: Double
              23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POSITION IN GENOME:
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ZIP: 53711-5399
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APPLICANT:
APPLICANT:
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CLONE: G
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                Matches
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                                                                                                                                                      RESULT 5
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GENERAL INFORMATION:
APPLICANT: Richards, Cynthia Ann
APPLICANT: Huber, Brian E.
TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
Patent No. 6194211
TITLE OF INVENTION: Antigen for Expression Targeting
FILE REFERENCE: PB1508USM
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ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
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LOCATION: 196..350
OTHER INFORMATION: /note= "Nucleotides 196-350 are
OTHER INFORMATION: unique flanking sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /note= "Nucleotides 110-195 are OTHER INFORMATION: repeat sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1..109
OTHER INFORMATION: \(\note=\)"Nucleotides 1-109 are
OTHER INFORMATION: \(\note=\)"nique flanking sequence"
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GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ACID HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: UMBER: US/09/738,894A
CURRENT APPLICATION NUMBER: US/09/738,894A
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
1.0%; Score 22; DB 4; Length 36651;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 22; Conservative 0; Mismatches 0; Indels (
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TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08724394A
Fatent No. 5872237
                                                                                ; Sequence 3, Application US/09738894A; Patent No. 6331423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3
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Kronmal, Gregory S.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
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TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
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INFORMATION FOR SEQ ID NO: 20:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
LENGTH: 36651
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                                                      US-09-738-894A-3
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APPLICANT:
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APPLICANT: Richards, Cynthia
TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (CEA
TITLE OF INVENTION: Transcriptional Regulatory Region
FILE REFERENCE: PB1087US4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Huber, Brian
APPLICANT: Huber, Brian
APPLICANT: Huber, Brian
APPLICANT: Richards, Cynthia
TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Regu
TITLE OF INVENTION: Sequence
FILE REFERENCE: PB10870S3
CURRENT APPLICATION NUMBER: 08/08/154,712B
CURRENT FILING DATE: 1993-11-19
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
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Pred. No. 3.3;
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100.0%; Pred. No. 3.3;
ive 0; Mismatches 0; Indels (
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Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/08481968A ; Patent No. 6300490
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100.0%; Pre
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Best Local Similarity 100.0
Matches 22; Conservative
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Matches 22; Conservative
SOFTWARE: Patentin Ver.
                                                                                ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                         11288
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                                                                                                    US-08-646-301A-1
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                                                             TYPE: DNA
                  SEQ ID NO 1
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Best Local Similarity 100.0
Matches 22; Conservative
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US-08-724-394A-22
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                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                       1.0%; Score 22; DB 2;
100.0%; Pred. No. 2.6;
tive 0; Mismatches
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFEMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fitts, Renee A. REGISTRATION UNDBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                    Db 236746 CAGCCTGGGTGACAGTGAGACT 236767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kronmal, Gregory S. APPLICANT: Lauer, Peter M. APPLICANT: Ruddy, David A. APPLICANT: Thomas, Winston APPLICANT: Tsuchihashi, Zenta APPLICANT: Wolff, Roger K.
        SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
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LENGTH: 246240 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 22; Conservative
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STRANDEDNESS: not r
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Sequences and Antibodies Thereto
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                  0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/724,394A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 22; DB 2;
100.0%; Pred. No. 2.6;
100.0%; Pred. No. 2.6; tive 0; Mismatches
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 017957-000100 TELECOMMUNICATION: TELECHONE: 415-576-0200 TELEFHONE: 415-576-0300
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....ber: US/08/724,394A
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 236746 CAGCCTGGGTGACAGTGAGT 236767
                                                                                                                                                                                        Sequence 22, Application US/08724394A Patent No. 5872237
                                                                               Db 236746 CAGCCTGGGTGACAGTGAGACT 236767
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100.0%; Pir
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APPLICANT: Kromal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fitts, Renee A. REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                            APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                        28 CAGCCTGGGTGACAGTGAGACT 49
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LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                  GENERAL INFORMATION:
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us-09-667-170a-440.oli.rni

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APPLICANT: Robison, Keith E.

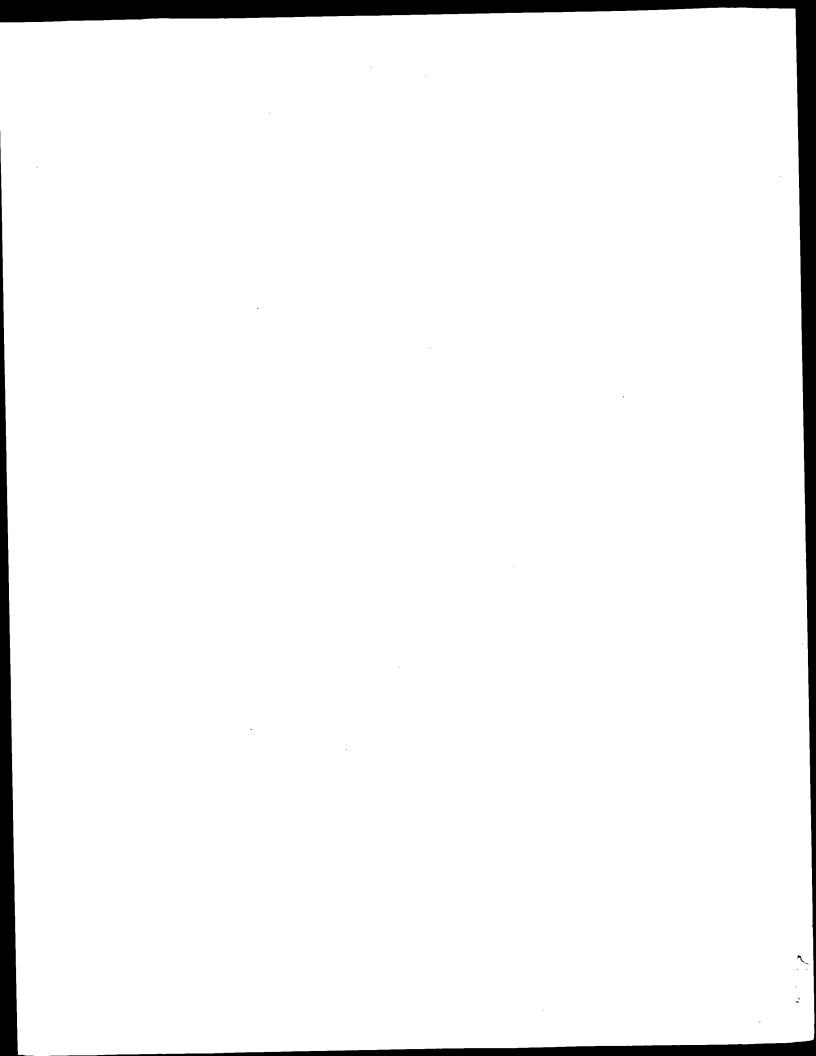
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs CLEREPERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
NUMBER OF SEQ ID NOS: 268
SOFWARE: PatentIn Ver. 2.0
SEQ ID NO 247
LENGTH: 544
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APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Astle, Jon H.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Gario, Theodore J.
APPLICANT: Lewis, Marcia E.
APPLICANT: Lewis, Marcia E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE REFERENCE: CCD-257 (US)
CURRENT FILING DATE: 1999-06-08
EARLIER RPLICATION NUMBER: US 60/088,801
CURRENT FILING DATE: 1999-06-10
SOFTWARE: FERSEREY FOR OF SEX ID NOS: 850
NUMBER OF SEX ID NOS: 850
SOFTWARE: FRASEREY FOR WINDOWS: SOFTWARE: SAND CARSION STAND STAN
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0.9%; Score 21; DB 4; Length 544;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels
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0.9%; Score 21; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels
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; LOCATION: (1)..(544)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-247
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: LOCATION: (579)

: OTHER INFORMATION: n = A,T,C or G

US-09-328-111-68
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 579
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Search completed: April 16, 2003, 14:34:09 Job time: 1441 secs



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9736.858 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence 440, App Sequence 441, App Sequence 411, App Sequence 31, Appl Sequence 39, Appl Sequence 39, Appl Sequence 37, Appl Sequence 37, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 53, Appl Sequence 130, Appl Sequence 130, Appl Sequence 1307, Appl Sequence 2201, Appl
SUMMARIES 3 ID	10. US-09-854-133-440 10. US-09-738-973-440 10. US-09-854-133-441 10. US-09-738-973-441 10. US-10-163-866-30 10. US-10-163-866-30 10. US-10-163-866-30 10. US-10-163-866-32 10. US-10-163-866-32 10. US-10-163-866-32 10. US-10-163-866-32 10. US-10-163-866-32 10. US-10-163-866-32 10. US-09-874-133-442 10. US-09-878-1307 10. US-09-878-1307 10. US-09-988-598-2201
% Query Match Length DB	2239 2239 2239 1239 13144 1642 1642 1642 1642 1642 1646
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Score	2233 2239 1867 1867 1722 1450 1420 1420 1420 1239 1239 415 281 107 107
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Sequence 108, App Sequence 1606, Ap Sequence 1606, Ap Sequence 6384, Ap Sequence 298, Ap Sequence 216, App Sequence 292, App Sequence 292, App Sequence 286, App Sequence 286, App Sequence 31, App Sequence 2780, App Sequence 1, Appli Sequence 11, Appli	CANCER	th 2239; .s 0; Gaps 0;
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8-108 4-1606 47-1606 01-5938 01-5938 01-5958 01-2998 01-2998 01-2998 01-2998 01-2998 01-2992 01-2986 01-2922 01-2986 01-2922 01-2986 0	FOR IS OF	DB 9
US-09-974-298-108 US-10-092-154-1606 US-09-764-847-1606 US-09-867-701-5958 US-09-867-701-2998 US-09-933-797-216 US-09-924-035A-346 US-09-924-035A-346 US-10-078-090-6 US-10-078-090-6 US-10-108-605-286 US-09-764-855-292 US-09-764-872-813 US-09-764-877-3955	METHODS FOR DIAGNOSIS OF ,133	2239; No. 0; latches
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2540 8894 8894 8894 1356 492 594 1023 6427 11184 31718 31718 4239 90014 487 948 1260 1260 1260 1398 3563 55795	pplication US/0985 US200201834991 TON: "s, Michael J. "amath, Radoh derson, Robert A. son, Darin R. rist, Heather Tist, Heather TON: THE THERAPY 21012.147510 DAYE: 2001-05-11 D NOS: 735 EQ for Windows Ver	100.0% 100.0% vative
	m Hoteephing is	Match 100 Local Similarity 100 Les 2239; Conservative
	RESULT 1 US-09-854-133-440 ; Sequence 440, Appli, sequence 440, Appli, publication No. US2; GENERAL INFORMATION APPLICANT: Lodes, APPLICANT: Henderr, APPLICANT: Benson APPLICANT: Benson APPLICANT: Benson TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION CURRENT APPLICATION CONTACTION CONTACTION CONTACTION CONTACTION CURRENT APPLICATION CONTACTION CONTACT	ch 1 Simi 239;
- ···	SULT 1 -09-854-133 Sequence 44 Publication GENERAL INF APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF II TITLE OF II FILE REFER CURRENT FII WUMBER OF SOFTWARE: B SOFTWARE: B LONGHEN TELL LONGHEN TELL FILE REFER CURRENT FII CUR	Query Match Best Local Matches 223
22222222222222222222222222222222222222	RESULT 1 US-09-854 ; Sequence ; Sequence ; GENERAL APPLICC; APPLICC ; APPLICC ; APPLICC ; APPLICC ; APPLICC ; TITLE (FILE R ; TITLE (FILE R ; CURRENI ; NUMBER ; SOFTWARF ; SOFTWARF ; TYPE;	Query M Best Lo Matches
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Patent No. US20020110563A1
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Henderson, Robert A.
Lodes, Michael J.
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APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Benson, Darin R.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
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APPLICANT: Mannion, Tane
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.4756
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CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFWARE: FRAKISED for Windows Version 3.0
SEQ ID NO 440
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Fling, Steven P.
Mohamath, Raodoh
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Matches 2239; Conservative
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APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG
TITLE OF INVENTION: THE THERREY AND DIAGNOSIS OF LUNG
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
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; Publication No. US20020183499Al
; GENERAL INFORMATION:
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                                             1714 CCAGAAGAAAGATAAGTAATGAACTAGACTTGAGATCTTGGCAATCTGCCCAAGGGGA 1773
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APPLICANT: Hing, Steven P.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Secrist, Heather
APPLICANT: Berist, Carol Yoseph
APPLICANT: Biliot, Mark
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Allos, Michael D.
TITLE OF INVENTION: THE THERAPY AND DIACNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
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CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FASTSEQ for Windows Version 3.
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; Patent No. US20020110563A1
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Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
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ORGANISM: Homo sapiens
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100.0%; Pred. No. v.
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EXO2 080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
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CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FLING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/10163866
Publication No. US20030027188A1
GENERAL INFORMATION:
APPLICANT: EXELIXIS
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1866; Conservative 0; Mismatches
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                SEQ ID NO 31
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JOHNSTAIL THE CALLIAIS.

APPLICANT: EXELIXIS. INC.

TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

FILE REFERENCE: EXO2-080C

CURRENT APPLICATION NUMBER: US/10/163,866

CURRENT FILING DATE: 2002-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR PELING DATE: 2001-06-05

PRIOR PAPLICATION NUMBER: US 60/298,605

PRIOR PELING DATE: 2001-10-10

PRIOR PAPLICATION NUMBER: US 60/398,733

PRIOR FILING DATE: 2001-10-22

PRIOR PAPLICATION NUMBER: US 60/397,253

PRIOR APPLICATION NUMBER: US 60/357,600

PRIOR PRILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PARENTLY OF THE P53 PATHWAY AND METHOR PRILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 54
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                   Sequence 29, Application US/10163866 Publication No. US20030027188A1
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                                                      GENERAL INFORMATION:
US-10-163-866-29
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US-10-163-866-29
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Matches 1772;
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GURREAL INCOMATICANT: EXELIXIS, INC.

TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REPERENCE: EXO2-0605
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
PRIOR PAPLICATION NUMBER: US 60/296,076
PRIOR PLILING DATE: 2001-06-05
PRIOR PLILING DATE: 2001-10-10
PRIOR PLILING DATE: 2001-10-10
PRIOR PLILING DATE: 2001-10-10
PRIOR PLILING DATE: 2001-10-12
PRIOR PLILING DATE: 2001-10-22
PRIOR PLILING DATE: 2001-10-15
PRIOR PLILING DATE: 2001-10-15
PRIOR PLILING DATE: 2002-02-15
PRIOR PLING DATE: 2002-02-15
PRIOR PLING DATE: 2003-03-17
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                                                                                                                                                                                                                                                                                                               Sequence 30, Application US/10163866 Publication No. US20030027188A1 GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 1504; Conservative 0
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APPLICANT: EXELIXIS,
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REPERENCE: EX02-080.
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
PRIOR PELICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-2
PRIOR FILING DATE: 2001-10-2
PRIOR FILING DATE: 2001-0-215
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
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                ; Sequence 33, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
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US-10-163-866-33
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LENGTH: 1542
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APPLICANT: EXELIXIS, INC.

TITLE OF INVENTION: SLC78 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-05
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-110-10
PRIOR FILING DATE: 2001-10-12
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100.0%; Pred. No. 0;
Live 0; Mismatches
                  60/357,600
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
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                                                                                                                          TYPE: DNA
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TITLE OF INVENTION: SLC78 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-080C
CURRENT APPLICATION NUMBER: US,10/163,866
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US,60/296,076
PRIOR PELION NUMBER: US,60/298,605
PRIOR APPLICATION NUMBER: US,60/328,605
PRIOR APPLICATION NUMBER: US,60/338,733
PRIOR APPLICATION NUMBER: US,60/338,733
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: US,60/357,253
PRIOR PILING DATE: US,60/357,600
PRIOR PILING DATE: US,60/357,600
PRIOR PILING DATE: US,60/357,600
PRIOR APPLICATION NUMBER: US,60/357,600
PRIOR PILING DATE: 2002-02-15
PRIOR PILING DATE: 2002-02-15
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1081 TCATTAGCAGITCCGAICTITGTIGCCCTCTCCTGCTITGGCTCCATGAACGGTGTGTG 1140
                             1234 ITTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
                                              1141 TITGCIGICICCAGGITALICTATGTIGCGICICGAGAGGGTCACCTICCAGAAAICCTC 1200
                                                                                         1294 TCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTG 1353
                                                                                                         1201 TCCATGATTCATGTCCGCAAGCACACTCTTCTACCAGCTGTTATTGTTTTGCACCCTTTG 1260
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Publication No. US20030027188A1
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NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
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994 ACTGAAGAAGTAGAAAACCCTGAAAAACCATTCCCCTTGCAATATGTATATCCATGGCC 1053
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                                                                                                                 514 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 573
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188 ACCATCATTGGAGCAGGAATCTTCATCTCCTAAGGGGGGTGCTCCAGAACACGGGCAGC 247
                                                              308 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 367
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Thu Apr 17 09:48:28 2003

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TITEL OF INVENTION: SLOPE

TITLE REFERENCE: EX02-080C

CURRENT APPLICATION NUMBER: US/10/163,866

CURRENT FILING DATE: 2002-06-05

PRIOR APPLICATION NUMBER: US 60/296,076

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR PRIOR APPLICATION NUMBER: US 60/328,605

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 54

SCOTT NO. 53
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                      1328 CTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1387
                                                                                   1594 ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTATGGGACAAGAAACCCAGG 1653
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1534 CTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1593
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Matches 868; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC78 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-080C
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                                                                                                                                    908 GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTC 967
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694 ATTCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 753
                GTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACC
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Matches 415; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR PLICATION NUMBER: US 60/328,605
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR PLING DATE: 2001-10-10
PRIOR PLING DATE: 2001-10-22
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 54
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; Publication No. US20030027188A1
; GENERAL INFORMATION:
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US-10-163-866-32
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                                                                           CCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAACCATTTTTT 693
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APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475c10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 12.6%; Score 281; DB 9; Length 337; Similarity 100.0%; Pred. No. 3.8e-133; B1; Conservative 0; Mismatches 0; Indels
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Publication No. US20020183499A1
GENERAL INFORMATION:
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61 AGAATTAAGGAAAAAAAAAAAAAAAAAAAGAGAGGAGGAAATTCCAGGCCAATTGTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.6%; Score 281; DB 10; Length 337; 100.0%; Pred. No. 3.8e-133; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Barlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C1
CORRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 AGGCTGCCTTCCCTGGGCAACAAGGAGCACCTGGGCAGGA 284
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                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1307, Application US/10046935; Patent No. US20020156011A1
                                         ; Sequence 442, Application US/09738973
; Patent No. US20020110563A1
                                                                                                                                                                                                          APPLICANT: Algate, Paul A.
APPLICANT: Secrist, Heather
APPLICANT: Indirias, Carol Yoseph
                                                                                                      Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
                                                                                                                                                                                                                                                                 APPLICANT: Benson, Darin R. APPLICANT: Elliot, Mark APPLICANT: Mannion, Jane APPLICANT: Kalos, Michael D.
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; ORGANISM: Homo sapiens
US-09-738-973-442
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                                                                                GENERAL INFORMATION:
APPLICANT: Reed, St
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RESULT 14
US-09-738-973-442
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US-10-046-935-1307
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om nucleic - protein search, using frame_plus_n2p model

Run on:

April 16, 2003, 14:10:10 ; Search time 71 Seconds (without alignments) 8404.173 Million cell updates/sec

US-09-667-170A-440 Title:

Perfect score: Sequence:

BLOSUM62 Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

Database

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:* /gcgdata/geneseq/geneseqp-embl/AA1992.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:* DAT: * . DAT: * /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1998.DAT:* /gcgdata/geneseq/geneseqp-embl/AA1999.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /SIDS2/gcqdata/geneseq/geneseqp-embl/AA1982.bAT:*/SIDS2/gcqdata/geneseq/geneseqp-embl/AA1983.bAT:*/SIDS2/gcqdata/geneseq/geneseqp-embl/AA1984.bAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*/SIDS2/gcgdata/geneseq/geneseq-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqy/geneseqy/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqy/gen /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997 A_Geneseq_101002:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scription	Human c	EST encode	n L-typ	L-type a	eutral amin	ıgnt 201	amino aci	-duom	mela		Drosophila melanog	ORFX	٠,	r phila	Human amino acid t	Drosophila melanog	hydr	acid		phila mela	secreted pr	pancreati	Nowel human diagno	ElfH pro	hydrophob	tumour-ass		polypept	de #518	Times been expres	numan bone marrow Dentide #5058 enco	#5121	peptide	noc	_ 0	nterococcus fa	nterococcus f	cus	⇉		Arabidopsis thalia
SUMMARIES	ID	ABB119	391	8248	8248	AAY 584 26	ABB12114 AAV41159	AAY27076	AAY87630	ABB58292	AAB72393	ABB71209	AAB43135	AAR72395	ABB62049	ABB11788	ABB62891	AAB88569	AAG63803	AAG63804	ABB64405	AAY915/6	AAB34293 AAV91451	ABG12125	AAB10289	AAB88577	AAW80803	ABB90268	ABB90216	ABB3/681	AAM70796	AAM18624	AAM31084	ABG40523	355	387	343	3506	2995	2220	2220	220
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ALIGNMENTS

Human cystine/Glu transporter homologue, SEQ ID NO:2327. ABB11957 standard; peptide; 521 AA (first entry) 11-JAN-2002 ABB11957; RESULT 1 ABB11957

Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; prolliferation; metastasis; cancer; tumour; haematopoietic disorder; prolliferation; metastasis; cancer; tumour; haematopoietic disorder; exthmis atherios cell disorder; asthmis athritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;

bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder;

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cell culture; drug screening; gene therapy; antiinflammatory; antiathmatic; antiathritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
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Homo sapiens.

WO200157188-A2.

09-AUG-2001

05-FEB-2001; 2001WO-US03800

03-FEB-2000; 2000US-0496914.

27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC.

rang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49. N-PSDB; ABA09201

or ameliorating a medical condition in a mammalian subject Human proteins and DNA encoding sequences useful for preventing, e.g. arthritis and cancer -

Claim 20; Page 286; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. The polypeptides, methods of detecting the nucleotides against the polypeptides, methods of detecting the nucleotides. The polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; has activity; tissue growth activity; has memanopolesis regulatory activity; tissue growth activities; memanomodulatory activity; activin- or inhibin-related activities; chemotactic or chemotyperior activities; haemastopatic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their bolodical activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., imyeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthitis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial isofamenta, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.

Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells and received the annipulate can be used to reconstince and proved factor activity may be used to an encoding them and the statement of viral and the statement of any polypeptides may be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.

Conservative: Matches 3.36e-276 2519.00 96.51% 521 AA; Percent Similarity: Alignment Scores:

1084 GTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGTG 1143 1144 ACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTC 1203 1024 ATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAAT 1083 843 904 TCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTATGCA 963 184 AAGCCTGTTGTGTCCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGAGG 243 244 CTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACGCC 303 CCTAAGGGGGGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTG 483 TTTGGACGCTACATTCTGGAACCATTTTTTATTCAATGTGAAATCCCTGAACTTGCGATC 723 944 ATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCCTTT 903 246 SerGlyArgAspSerSerIleThrArgLeuProLeuAlaPheTyrTyrGlyMetTyrAla 265 304 TTTTCAGGAAGAGGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGAAGTCACT 363 364 TTACTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCT 423 86 ProLysGlyValLeuGlnAsnThrGlySerValGlyMetSerLeuThrIleTrpThrVal 105 24 LysProValValSerThrIleSerLysGlyGlyTyrLeuGlnGlyAsnValAsnGlyArg 43 66 LeuLeuArgGlyValSerIleIleIleGlyThrIleIleGlyAlaGlyIlePheIleSer 85 544 AAAICIGGAGGICATIACACATATITIGGAAGICITIGGICCAITACCAGCITITGIA 504 CGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGCA 724 AAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGC 784 TGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATAATT TATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCTGAAAAAACC TGTGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAG 188 Indels: (1-2239) x ABB11957 (1-521) 96.51**%** 61.1**4%** Best Local Similarity: US-09-667-170A-440 Query Match: 126 664 124 δλ q δλ δy q Óλ Db ολ qq οy Db δλ d qq Q qq ò qq Op Qγ δλ ДQ Пр qq ŏ qq δ δλ οy δy q ŏ g δ

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CTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGACCTC 1383
                                                                                                                                                            GGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTG 1503
                                                                                                                                                                                                   TICATCCCAGCITIGITITCCTICACAIGCCTCTICAIGGITGCCCTITICCCTCTATICG 1563
                                                                                                                                                                                                                                          GACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATTAT 1623
                                                                                                                                                                                                                                                                                   CTCTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACC 1683
           TCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTGCG
                                        TCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCT
                                                                                        GACAGTCTTTTGAATTTCCTCAGTTTTTGCCAGGTGGCTTTTTTATTGGGCTGGCAGTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; hc tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; blodiversity; gene therapy; nutrition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Human EST encoded protein SEQ ID NO: 1439.
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                                                                                                                                                                                                                                                                                                                                                                                   AAM23914 standard; Protein; 424 AA.
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                    The present invention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                                                                                                               520 GCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTC 579
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Mismatches:
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                                      Claim 20; Page 1001-1002; 1275pp; English.
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                                                                                                                                                                       1420 CITITIATIGGCCIGGCAGIIGCIGGCTGAITIAICIICGAIACAAAIGCCCCAGAIAIG 1479
                                                                                    ATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATG 1359
                                                                                                                                                                                                                                                                                 380
                                                                                                                                                                                                                                                                                                                241 AlaValProIlePheValAlaLeuSerCysPheGlySerMetAsnGlyGlyValPheAla 260
                                                    Human L-type amino acid transporter 1 protein sequence SEQ ID NO:2.
                                                                                                                                                                                                                             CTGACTGGAGTCCCTGCGTATTATCTCTTTTATTATGGGACAAGAAACCCAGGTGGTTT
1180 GCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCT
                                           1240 GTCTCCAGGTTATTCTATGTTGCGTCTCCGAGAGGGTCACCTTCCAGAAATCCTCCATG
                                                                                                                                                                                                                  CATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-type amino acid transporter 1; LAT1; 4F2hc; 4F2 heavy chain; neutral amino acid transporter; tumour; cancer; proliferation; cell membrane surface 4F2 molecule; anticancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY82488 standard; Protein; 507 AA.
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The present invention describes a cell surface protein which is an L-type amino acid transporter-1 (LAT1), which mediates the transport of neutral amino acids, leucine, isoleuchne, phenylalamine, methionine, tyrosine, tryptophan, valine and histidine, into the cell independently of sodium ions. The LAT1 protein conjugates with the cell membrane surface molecule 4F2. Antisense DNA or RNA, antibodies, antibodies, fragments, and peptide and non-peptide antagonists to LAT1 are useful as anticancer agents. The present sequence represents human LAT1, which is specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACGCTACATTCTGGAACCATTTTTATTCAATGTGAAATCCCTGAACTTGCGATCAAG 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 LeuValAlaCysLeuCysValLeuLeuThrAlaValAsnCysTyrSerValLysAla 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 LeuLeuGlyPheValGlnIleGlyLysGlyAspValSerAsnLeuAspProAsnPheSer 232
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              membrane protein 4F2 and operates independently of sodium ions is useful for screening potential cancer proliferation inhibitors -
acid transporter protein which conjugates with cell
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961 GCATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAA 1020
                                                                                                1021 ACCATICCCCTIGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGGTGACA 1080
                                                                                                                                                         1081 AATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCA 1140
                                                                                                                                                                                                                  1141 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCC 1200
                                                                                                                                                                                                                                                                         1201 CTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCCAGGTTATTCTATGTT 1260
                                                          1261 GCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACAT 1320
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1621 TATCTCTTTATTATATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAAAA 1680
                                                                                                                                                                                                                                             313 ValAspPheGlyAsnTyrHisLeuGlyValMetSerTrplleIleProValPheValGly 332
                                                                                                                                                                                                                                                                                        373 ProValProSerLeuValPheThrCysValMetThrLeuLeuTyrAlaPheSerLysAsp 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat L-type amino acid transporter 1 protein sequence SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-type amino acid transporter 1; LAT1; 4F2hc; 4F2 heavy chain; neutral amino acid transporter; tumour; cancer; proliferation; cell membrane surface 4F2 molecule; anticancer.
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The present invention describes a cell surface protein which is an 1-type amino acid transporter-1 (LAT1), which mediates the transport of neutral amino acids, leucine, isoleucine, phenylalanie, methionine, tyrosine, tryptophan, valine and histidine, into the cell independently of solium ions. The LAT1 protein conjugates with the cell membrane surface molecule 4E2. Antisense DNA or RNA, antibodies, antibody fragments, and peptide and non-peptide antagonists to LAT1 are useful as anticancer agents. The present sequence represents rat LAT1, which is specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 GACGCCTTTTCAGGAAGAGGCCTTTTCAGGAAGAGAAAGTGCAGCTGAAGAGAAA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 LeuValPheAlaThrTyrLeuLeuLysProValPheProThrCysProValProGluGlu 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neutral amino acid transporter protein which conjugates with cell
                                                                                                                                                                                                                                  membrane protein 4F2 and operates independently of sodium ions is useful for screening potential cancer proliferation inhibitors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 ACGGTGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTTTATGCTGAATTGGGAACAACT
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This sequence represents a rat neutral amino acid transporter, LAT1. It interacts with a 520 amino acid protein (AAYS0427) to effect neutral amino acid transport. LAT1 is predicted to have up to twelve transmembrane domains from hydropathy analysis. The protein, and nucleic acids encoding it are useful for the in vitro analysis of drug permeation through cell membranes and blood tissue barriers.
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                                     Rat; neutral amino acid transporter; LAT1; drug permeation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Rat neutral amino acid transporter LAT1
                                                                                                                                                                                                                                                                                                               (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 9; 17pp; Japanese.
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47.618
29.228
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Best Local Similarity:
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                                                                                             Rattus sp.
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1000 GAAGTAGAAAACCCTGAAAAACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTC 1059
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                                       171 AlaAlaLysLeuValAlaCysLeuCysValLeuLeuLeuThrAlaValAsnCysTyrSer 190
                                                                                                                     191 ValLysAlaAlaThrArgValGlnAspAlaPheAlaAlaAlaAlaLysLeuLeuAlaLeuAla 210
                                                                                                                                                                                                        211 LeullelleLeuLeuGlyPheIleGlnMetGlyLysAspIleGlyGlnGlyAspAlaSer 230
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718 GCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGT 777
                                                                                                                                                                 838 ATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAA-------GGTCAAACGCAG 885
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411 LeuCysValalaLeuAlaIleIleGlyMetMetTrpLeuArgPheLysLysProGluLeu 430
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cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                 bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                   haematopoleeis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopath; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                       Human 4F2 light chain homologue, SEQ ID NO:2484.
           ABB12114 standard; peptide; 507 AA.
                                                                                                                                                                                                                        antifungal; vulnerary; antiulcer.
                                                    (first entry)
                                                                                                                                                                                                                                             Homo sapiens.
                                                   11-JAN-2002
                               ABB12114;
ABB12114
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09-AUG-2001.

05-FEB-2001; 2001WO-US03800.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49.

N-PSDB; ABA09358

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -

Claim 20; Page 308-309; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The Invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, or polypeptides, methods of identifying compounds which indides against the polypeptides, methods of identifying compounds which polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell alfernitation activities; stem cell growth factor activity; immunomodulatory activity; activity; tissue growth activities; chemicatelic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, hemmatopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and

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GCATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCTGAAAAA 1020

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repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithalial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 LeuLysGlyValAlaValIleValValAlaIleMetGlySerGlyIlePheValThrPro 72
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Mismatches:
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1140.00
66.17%
46.09%
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Best Local Similarity:
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173 LeuValAlaCysLeuCysValLeuLeuLeuThrAlaValAsnCysTyrSerValLysAla 192

LeuLeuGlyPheValGlnIleGlyLysGlyAspValSerAsnLeuAspProAsnPheSer 232

GTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAAGACGCCTTTTCA

233 PheGluGlyThrLysLeuAspValGlyAsnIleValLeuAlaLeuTyrSerGlyLeuPhe 252

-----GGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTAT

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autoimmune disorder; anemia; asthma; atherosclerosis; diabetes mellitus; multiple sclerosis; osteoarthritis; osteoporosis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferation disorder; human.
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                                              1021 ACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACA 1080
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                                                                                                                                          313 ValAspPheGlyAsnTyrHisLeuGlyValMetSerTrpIleIleProValPheValGly 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 LysThrThrProTrpSerValAlaSerAspPheThrIleIleLeuSerGlyLeuProVal 472
                                                                   253 AlaTyrGlyGlyTrpAsnTyrLeuAsnPheValThrGluGluMet1leAsnProTyrArg
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Hillman JL;
(INCY-) INCYTE PHARM INC
        WPI; 1999-633325/54
    Corley NC,
           N-PSDB; AAZ23240
    Yue H,
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treatment and prevention of cancer, inflammatory/autoimmune disorders and cell proliferation disorders -

Claim 1; Fig 1A-F; 32pp; English.

This represents a human amino acid permease homolog (AAPH). The AAPH nucleic acid, protein, AAPH (ant)agonists are useful in the diagnosis, treatment and prevention of cancer such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid or uterus; inflammatory/autoimmune disorders such as AIDS, Addison's disease, adult respiratory distress sydrome, alleries, ankylosing spondylitis, amyloidosis, anemia, emphysema, multiple sclerosis, osteoarthritis, osteoporosis, rheumatoid arthritis, ulcerative colitis, viral, bacterial, fungal, parasitic, protozoal infections; and cell proliferation disorders such as actinic, keratosis, cirrhosis, arteriosclerosis, myelofibrosis, and primary thrombocythemia. asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, cholecystitis, contact dermatitis, diabetes mellitus, Crohn's disease, atopic dermatitis, dermatomyosistis,

511 AA; Sequence

511 Length: 1.05e-118 Alignment Scores: Pred. No.:

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1149
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                                                                                                                                    850 CCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAAGACGCCTTTTCAGGA
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This sequence represents a human amino acid permease homologue (AAPH). The protein can be expressed by standard recombinant methodology, AAPH polynucleotides and polypeptides are useful for diagnosis, treatment and prevention of cancer e.g. adenocarcinoma, lung cancer, ovarian cancer; inflammatory/autoimmune disorders e.g. AIDS, Crohn's disease, rheumatoid arthritis; and cell proliferation disorders e.g. arteriosclerosis, psoriasis, hepatitis. AAPH polynucleotides are useful in gene therapy, in PCR-based methods for detecting upstream sequences, and also for generating hybridisation probes for mapping the naturally occurring
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                                                                                                                     Amino acid permease homologue; AAPH; cancer; inflammatory disorder; autoimmune disorder; cell proliferation disorder; adenocarcinoma; AIDS; Crohn's disease; rheumatoid arthritis; arteriosclerosis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human amino acid permease homolog (AAPH) polynucleotide and its complement useful for prevention and treatment of cancer, autoimmune and cell proliferation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 GTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCT
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                                                            Human amino acid permease homologue (AAPH).
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18-OCT-1999
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This invention describes a novel protein MONP-2 (I) and its encoding gene monp-2 (II) with a cell proliferation promoting effect isolated from a human peripheral blood. The new protein (I) and gene are useful in studying the expression abnormality and dysfunction of (I) as well as maintenance of immune function and development of drugs for e.g. immune diseases and cancers. This represents encodes the MONP-2 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel gene monp-2 encoding monocyte-specific protein with cell proliferation promoting effect, useful in studying its expression and immune function, and in developing drugs for e.g. immune diseases and
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                                                                                                                                                                                                              Human; monp-2; cell proliferation; drug development; immune disease;
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                                                                                        AAY87630 standard; Protein; 511 AA
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                                                                                                                                                                                   Human monp-2 protein.
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490 GTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                             1630 ATT-----ATATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACC 1683
              1570 ITIAGIACAGGGAIIGGCIICGICAICACTCIGACIGGAGICCCIGCGIAIIAICICIII 1629
                                                      441 IleasnSerLeuileGlyIlealaIlealaLeuSerGlyLeuProPheTyrPheLeuIle 460
                                                                                                                                   461 IleArgValProGluHisLysArgProLeuTyrLeuArgArgIleValGlySerAlaThr 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 1668; 21pp + Sequence Listing; English.
                                                                                                                                                                             1684 AGAACATTACAAATAATA---CTGGAAGTTGTACCAGAAGAAGAT 1725
                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 1668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-667-170A-440 (1-2239) x ABB58292 (1-505)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                     ABB58292 standard; Protein; 505 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PWD,
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1113.50
64.50%
42.19%
27.03%
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL02395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                           ABB58292;
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                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                    ABB58292
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1255 TATGTIGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAG 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      955 AIGTAIGCAIAIGCIGGCIGITITACCICAACTITGITACIGAAGAAGIAGAAAACCCI 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1015 GAAAAAACCATTCCCCTTGCAATATGTATTCCATGGCCATTGTCACCATTGGCTATGTG 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1075 CIGACAAAIGIGGCCIACIITACGACCATIAAIGCIGAGGAGCIGCIGCITCAAAIGCA 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1135 GTGGCAGTGACCTTTTCTGAGCGCCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTT 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTTTCCTCCCAGGTTATTC 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 MetAlaAsnValSerPheTyrThrIleLeuSerProAspGluValMetGlySerSerAla 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 PheileilealaThrGlyValTyrGlnLeuTyrLeuGlyAsnThrGlnTyrPhe--- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    715 CITGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 AspserAlaArgLeuLeuAlaValCysCysIleLeuValLeuThrLeuIleAsnCysTrp 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      775 AGIGICAGCIGGAGCGCCCGGAICCAGAITITCITAACCITTIGCAAGCICACAGCAAIT 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTTTGTACGAGICTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATA 654
                                                                                                                                                                                                                                                                415 ITCATCTCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGGCATGTCTCTGACCAIC 474
                                                                                                                                                                                                                                                                                                                                                                                                  535 ACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGTCCATTACCA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 AGAGACGCCTTTTCAGGAAGACGCCTTTTCAGGAAGAGAAAGTGCAGCTGAAGAGG 354
                                                                                                                                                                355 AAAGTCACITTACTGAGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATC 414
                                                                                           48 LysMetSerLeuLeuAsnGlyCysThrVallleValGlySerIleIleGlySerGlyIle 67
                                                                                                                                                                                                                                                                                                                     87
11 SerSerArgLysSerSerIleValAsnGlyAsnGlyAspAlaSerAlaLysLeuThrAsn 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  895 GACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTTATTATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 ValLysAsnLeuProArgAlaIleAlaIleSerCysThrLeuValThrIleValTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 ValalaValThrTyrAlaGluArgAlaPheGlyMetLeuAlaTrpThrIleProValPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AspvalLysTrpAlaThrAlaValGlnAspIlePheThrTyrAlaLysLeuLeuAlaLeu
                                                                                                                                                                                                                                                                                                             475 TGGACGGTGTGGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACA
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This invention relates to a neutral amino acid transporter having broad substrate selectivity to neutral amino acids, and which is inactivated by an amino acid transport activating factor 4f2he (4f2 heavy chain). The neutral amino acid transporter and its gene are useful in in vitro analysis of permeation of drugs and poisons through cell membrane, blood and tissues. The present sequence represents the rat L-type amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neutral amino acid transporter; amino acid transport activating factor; 4F2hc; 4F2 heavy chain; drug permeation; poison; rat; LAT2; L-type amino acid transporter 2.
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                                                                                             1375 GGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTATTGGGTG
                                                                                                                                                                                                                            GCAGTIGCIGGGCTGATITATCTICGATACAAATGCCCAGATATGCATCGTCCTTTCAAG 1494
                                                                                                                                                                                                                                                                                                                                                            GIGCCACTGTICATCCCAGCTITGTTTTCCTTCACATGCCTCTTCATGGTTGCCTTTCC 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1555 CTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCT 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1615 GCGTATTATCTCTTTATTATATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAG 1674
                                                                                                                                                       386 SerAspilePheAlaLeuileAsnTyrValGlyPheAlaThrTrpLeuSerIleGlyVal 405
                                                                                                                                                                                                                                                                                           406 AlavalLeuCysLeuProTrpLeuArgTrpAlaClnProAsnLeuProArgProlleArg 425
                                                                                                                                                                                                                                                                                                                                                                                                                       426 ValProMetValPheProIleValTyrLeuIleAlaThrIlePheValThrValValPro 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 PheThrProThrProAlaValLeuAlaMetAlaLeuLeuSerMetLeuTyrLeuThrVal 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat L-type amino acid transporter 2 (LAT2) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1675 AAAATAACCAGAACATTACAAATAATACTGGAAGTTGTA 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        486 GlyLeuThrGlnValLeuGlnLysLeuMetMetValVal 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 17-18; 37pp; Japanese.
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transporter 2 (LAT2).

Alignment Scores:

Sequence

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964 TATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCTGAAAAAACC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1024 ATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAAT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIGGCCTACTITACGACCATTAATGCTGAGGAGCTGCTGTTTCAAATGCAGTGCAGTG 1143
                                                                                                                                                            202 ATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGAGGCTGCCTTCCCTGGGCAAC 261
                                                                                                                                                                                                                                                                                                                                                                                 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                     501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 SerTyrValLysAspIlePheGlyGlyLeuAlaGlyPheLeuArgLeuTrpIleAlaVal 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 LeuVallleTyrProThrAsnGlnAlaVallleAlaLeuThrPheSerAsnTyrValLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 GlnProLeuPheProThrCysPheProProGluSerGlyLeuArgLeuLeuAlaAla11e 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 CysLeuLeuLeuLhrTrpValAsnCysSerSerValArgTrpAlaThrArgValGln 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 AspilePheThralaGlyLysLeuLeuAlaLeuAlaLeuIleIleIleIleMetGlyValVal 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             862 CAGCTAATTAAAGGTCAAACGCAGAACTTT-------AAAGACGCCTTTTCA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 AsnPheGlnGluProAspIleGlyLeuValAlaLeuAlaPheLeuGlnGlySerPheAla 245
                                                                                                                                                                                                                                 262 AAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGACGCC 321
                                                                                                                                                                                                                                                                                                      122 ITTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGAAAGTCACTTTACTGAGGGGAGTCTCC 381
                                                                                                                                                                                  682 GAACCATTTTTTATTCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     742 GGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAG 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        802 AITITCTTAACCITITGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATG 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 GInIleCysLysGlyGlu------PhePheTrpLeuGluProLysAsnAlaPheGlu 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    907 GGA---AGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTATGCA 963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 AACACGGGCAGCGTGGGCATGTCTGACCATCTGGACGGTGTGTGGGGGTCCTGTCACTA
                                                                                                                                                                                                                                                                                                                                                                         382 ATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 ITTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTAC
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     533
224
100
168
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                                         Conservative:
                                                         Mismatches:
                      Matches:
                                                                          Indels:
     Length:
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTTTATTATATGGGACAAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACC 1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1564 GACCCATTTAGTACAGGGATTGGCTTCGTCACTCTGACTGGAGTCCCTGCGTATTAT 1623
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 1144 ACCTITICIGAGCGGCTACIGGGAAATITCTCATTAGCAGTICCGAICTITGTIGCCCIC 1203
                                                                       1204 TCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTGC 1263
                                                                                                                                              1264 TCTCGAGAGGGTCACCTTCCAGAAATCCTCCATGATTCATGTCCGCAAGCACACTCCT 1323
                                                                                                                                                                                                                   CTACCAGCIGITATIGITITIGCACCCTTIGACAAIGATAAIGCICTICICIGGAGACCIC 1383
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                          326 SerThrPheGlyGlyValAsnGlySerLeuPheThrSerSerArgLeuPhePheAlaGly 345
                                                                                                                                                                                                                                                                                                                            405
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                                                                                                                                                                                                                                                                                                                         386 TyrThrLeuIleAsnTyrValGlyPheIleAsnTyrLeuPheTyrGlyValThrValAla
                                                                                                                                                                                                                                                     366 IleProAlaLeuLeuPheThrCysLeuSerThrLeuLeuMetLeuValThrSerAspMet
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11-JUL-2000; 2000US-0614150.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences.
                                                                                                                                                                                                                                                                                              (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                            ID NO 40419; 21pp + Sequence Listing; English.
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                                                     Disclosure; SEQ
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interactions
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; codqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease;
                                                                                                                                   1045 TCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATT 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1285 GAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTG 1344
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                                                                                     312 GlyTyrMetSerTrpIleMetProPheAlaValAlaCysSerThrPheGlySerLeuAsn 331
|||:::
|SerTyrValGluAlaLeuPheThrLeuIleSerValSerGlyLeuLeuTrpMetArgTyr 411
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AAC AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activitiess such as: cytostatic; hepatotropic; vulnerary; artiporalatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; artidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the proteins and nucleic acids may be used to treat cancers; proliferative disorders, neurodegenerative disorders, osteoarthritis, graft disease, cardalovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoingmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
                    cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autofimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 AAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGACGCC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 4966-4968; 5507pp; English.
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05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                         31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                   99US-0127607
                                                                                                      thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAC77345
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                                                                                                                                                                                                                                                                                            108 SerTyrValLysAspIlePheGlyGlyLeuAlaGlyPheLeuArgLeuTrpIleAlaVal 127
                                                                                                           142 AACACGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGGTCCTGTCACTA 501
                                                                                                                                28 GlySerGlyGlyGlyGlyValAlaLeuLySLySGluIleGlyLeuValSerAlaCySGly 47
                                                       502 ITTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTAC
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antithyroid; immunosuppressive; thyromimetic; antidiabetic; nootropic; antidiartheic; neuroprotective; antidepressant; nephrotropic; nootropic; antibalminthic; protozoacide; antidepressant; nephrotropic; virucide; diagnosis; prevention; treatment; membrane transport disorder; epilepsy; Menkes disease; diabetes; Parkinson's disease; neurological disorder; Alzheimer's disease; depression; schizophrenia; immune disorder; allergy; inflammatory disorder; ANDS, Addison's disease; atheroscierosis; gout; Graves disease; Hashimoto's thyroiditis; microbial infection; cancer; cell proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane transport protein; MTRP-6; antiinflammatory; cytostatic;
1453 TATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCA 1512
                                                          1513 GCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTT 1572
                                                                                                                    1573 AGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATT 1632
                                                                                                                                                                              1633 ATATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACCAGAACATTA 1692
                 448 ValCysGlyIleGlyLeuAlaIleMetLeuThrGlyValProValTyrPheLeuGlyVal
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                                                                                                                                                                                                                                                       /note= "Phosphorylation site"
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The present sequence is a membrane transport protein,

MTRP-6 from Incyte clone 2414415 isolated from human HNT3AZTO1 cDNA

Library. WRRP-6 shows homology to human amino acid transporter and

SLC7A8. It is expressed in reproductive and nervous tissues.

The present sequence is useful in diagnosis, prevention and treatment
of disorders related with increased or decreased expression of MTRP
c such as familial goitre, Menkes disease, diabetes, Parkinson's disease,
c schizophrenia, immune/inflammatory disorders such as AlDS, Addison's
c helminthic infections and cell proliferative disorders such as cancer.
Fragments of WTRP polymucleotides are useful as targets in microarrays.

WTRP DNA is also useful for generating hypridisation probes useful in
c mapping genomic sequences and detecting differences in sequences among
c screening libraries of compounds in drug screening techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epilepsy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human membrane transport proteins useful for diagnosis, prevention and treatment of membrane transport disorders, immune/inflammatory disorders and cell proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                         Guegler KJ;
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                                   382 ATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCCTAAGGGCGTGCTCCAG 441
                                                                                                    442 AACACGGGCAGCGTGGGCATGTCTCTGACCGTGTGTGGGGGTCCTGTCACTA 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A neutral amino acid transporter having broad substrate selectivity useful for in vitro analysis of permeation of drugs and poisons through cell membranes, blood and tissues -
                                                                                                                                                                                                                                                                                                                                                                                            Neutral amino acid transporter; amino acid transport activating factor; 4F2hc; 4F2 heavy chain; drug permeation; poison; human; LAT2; L-type amino acid transporter 2.
                                                                                                                                                         1633 ATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACCAGAAAATTA 1692
                                                                                                     1573 AGTACAGGGATTGGCTTCGTCATCACTCTGGAGTCCCTGCGTATTATCTCTTTATT 1632
1453 TATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCA 1512
             428 IlelleTyrLeuLeuPheTrpAlaPheLeuLeuValPheSerLeuTrpSerGluProVal 447
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                                                                                                                                448 ValCysGlyIleGlyLeuAlaIleMetLeuThrGlyValProValTyrPheLeuGlyVal
                                                   1513 GCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTT
                                                                                                                                                                                                                                                                                                                                                                    Human L-type amino acid transporter 2 (LAT2) amino acid sequence.
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                                                                                             13 LysLysHisProGly-----GlyGlyGluSerAspAlaSerProGluAla 27
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US-09-667-170A-440 (1-2239) x AAB72395 (1-535)
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1333 GTAATTGTTTTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTT 1392
                                                                                                                  1393 TIGAATTICCICAGITTIGCCAGGIGGCITTITATIGGGCIGGCAGITGCIGGGCIGAIT 1452
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                                                                  368 LeuLeuPheThrCysIleSerThrLeuLeuMetLeuValThrSerAspMetTyrThrLeu 387
                                                                                                                                              448 ValCysGlyIleGlyLeuAlaIleMetLeuThrGlyValProValTyrPheLeuGlyVal 467
348 GlyHisLeuProSerValLeuAlaMetIleHisValLysArgCysThrProIleProAla 367
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874 GGTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG
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/translation="MYRKPVVSTISKGGYLQGNVNGRLPSLGNKEPPGQEKVQLKRKV
TLLRGVSIIIGTIIGAGIFISPKGVLQNTGSVGMSLTIWTVCGVLSLFGALSYAELGT
TIKKSGGHYTYILEVFGPLPAFVRVWVELLIIRPAATAVISLAFGRYILEPFFIQCEI
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Submitted (11-MAY-2000) Bassi M.T., Telethon Institute of Genetics
and Medicine, Via Olgettina 58, 20132 Milan, ITALY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/cell_line="NT2, undifferentiated teratocarcinoma cell
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                                   1774 GACACAAAATAGGGATTTTTACTTCATTTTCTGAAAGTCTAGAGAATTACAACTTTGGTG 1833
                                                       1834 AIAAACAAAAGGAGTCAGTTATTTTATTCATATATTTTAGCATATTCGAACTAATTTCT 1893
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Unpublished
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/protein_id="CAC81905.1"
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/db_xref="taxon:9606"
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QNFKDAFSGRDSSITRLPLAFYYGMYAYAGWFYLNFYTEEVENPEKTIPLAICISMAI
VTIGYVLTNYAYFTTINAEELLLSNAVAYFSERLLGNFSLAVPIFVALSCFGSMNGG
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SFARWLFIGLAVAGLIYLRYKCPDMHRPFKVPLFIPALFSFTCLFMYALSLYSDPFST
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PELAIKLITAVGITVVMVLNSMSVSWSARIQIFLTFCKLTAILIIIVPGVMQLIKGQT
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                                                                                                                                                                                                                                              GIGFVITLTGVPAYYLFIIWDKKPRWFRIMSEKITRTLQIILEVVPEEDKL"
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                                                                                  2857. .3127
/rpt_family="Sine/Alu"
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ONFKDAFSGRDSSITRLPLAFYYGMYAYAGWFYLNFVTEEVENPEKTIPLAICISMAI
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                                            PRI 02-MAY-2001
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                                    2482 bp mRNA linear PRI 02-MAY-200 Homo sapiens cystine/glutamate transporter xCT mRNA, complete cds. AF252872
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Chancy.C.D., Kekuda,R., Wang,H., Huang,W., Prasad,P.D., Smith,S.B.
                                                                                                                                                                                                                                                                                                                                          Wang, H., Prasad, P.D. and Ganapathy, V.
Direct Submission
Submitted (05-APR-2000) Biochemistry & Molecular Biology, Medical
College of Georgia, 1120 15th Street, Augusta, GA 30912, USA
Location/Qualifiers
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Transporter in Retinal Pigment Epithelial Cells
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/protein_id="AAK49111.1"
/db_xref="GI:13924720"
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AGC AGC
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GGCTTTTATTATGGAAT
aagaagtagaaaaccctgaaaaa
CACCATTGGCTATGTGCT
GCTGCTTTCAAATGCAGT
AGCAGTTCCGATCTTTGT
CTGTCTCCAGGTTATTCT
GATTCATGTCCGCAAGCA
GATAATGCTCTTCTCTGG
GCTTTTTATTGGGCTGG
GCATCGTCCTTTCAAGGTC
CATGGTTGCCCTTTCCCT
TCTGACTGGAGTCCCTGC
TAGAATAATGTCAGAGAAAA:
agaagataagttatgaac'
AAAATAGGGATTTTACTTCA

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL plate: 29 Row: g Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 5568544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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BC012087 GI:15082351
MGC.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2155)
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Submitted (02-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                          TCGCACAATTCTTGAGTCTCTGATACCTACTATTGGGGTTAGGAGAAAAGACTAGAAA 2013
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1777 GACACAAAATAGGGATTTTTACTTCATTTTCTGAAAGTCTAGAGAATTACAACTTTGGTG 1836
                                                    1834 ATAAACAAAAGGAGTCAGTTATTTTATTCATATATTTTAGCATATTCGAACTAATTTCT 1893
                                                                                2014 TTACTATGTGGTCATTCTCTACAACATATGTTAGCACGGCAAAGAACCTTCAAATTGAAG 2073
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/tissue_type="Kidney, renal cell adenocarcinoma"
/clone_lib="NIH_MGC_14"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC cancer Agency, Vancouver, BC, Canada
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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TLLRGYSIIGTIIGAGIFISPRGYLQNTGSYGMSLTIWTVCGVLSLFGALSYAELGT
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PELAIKLITANGITTYNWILNSWSYSMSARIOIFLTFCKLTALLIIIYPGYMOLIKGOT
ONFKDAFSGRDSSITRLPLAFYYGWYAYAGWFYLNFVTEEVENPEKTIPLAICISMAI
YIGYVLTWYNXYFTTINAELLLSNANAYTESERLLGNFSLAVPIFVALSCFGSWNGG
VFAVSRLFYVASREGHLEDFLISMIHVRKHTPLPAVILHPLTMIMLFSGDLDSLLNFL
SFARWLFIGLAVAGLIYLRYRCPDMHRFFYVDLFIPALFSFTCLFWYALSCFSSWGG
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/lab_host="DH10B-R"
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VFAVSRLFYVASREGHLDEILSMIHVRKHTPLPAVIVLHPLTMIMLFSGDLDSLLNFL
SFARWLEIGLAVAGILTYLRYKCPDMRPFKYPLFIPALFSFTCLFWYALSLYSDPFST
GIGFVITLIGVPAYYLFIIWDKKPRWFRINSEKITRTLQIILEVVPEEDKL"
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TLLRGVSIIIGTIIGAGIFISPKGVLQNTGSVGMSLTIWTVCGVLSLFGALSYAELGT
TIKKSGGHYTYILEVFGPLPAFVRVWVELLIIRPAATAVISLAFGRYILEPFFIQCEI
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                                                                           AF200708 1874 bp mRNA linear PRI 01-DEC-2000
Homo sapiens calcium channel blocker resistance protein CCBRl mRNA,
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                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 (bases 1 to 1874)]
Conklin, D. S. and Beach, D. H.
CCBRI, novel CD98 light chain implicated in redox control and
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Submitted (01-NOV-1999) Cold Spring Harbor Labs, 1 Bungtown Rd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="X-c transporter; CD98 light chain"
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/db_xref="taxon:9606"
/cell_line="fibrosarcoma HT1080"
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Conklin, D.S. and Beach, D.H.
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                                                                                                               874 GGTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG
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CCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAACCATTTTTT
                     694 ATTCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA
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Homo sapiens mRNA for cystine/glutamate transporter, complete cds. AB026891
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ONFKDAFSGROSSITRLPLARYYGWYAYAGWFYLNFVTEEVENPEKTIPLAICISMAI
VIGYVLTNVYFTTINAEELLLSNAVATFSERLLGARSLAYPIFYALSCFGSWNG
VFAVSRLFYVASREGHLPEILISMIHVRHTPLPAVIVLHPLTMIMLFSGDLDSLLNFL
SFARWLFIGLAVAGLIYLRYRCPDMHRPFKYDLFIPALFSFTCLFWYALSLYSDPFST
GIGFYITLTGVPAYYLEIIWDKKPRWFRIMSEKITRTLQIILEVVPEEDKL"
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TLLRGVSIIIGTIIGAGIFISPKGYLONTGSYGMSLTIWTYCGYLSLFGALSYAELGT
TIKKSGGHYTYILEVFGPLPAFVRVWYELLIIRPAATAVISLAFGRYILEPFFIQCEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1774 GACACAAAATAGGGATTTTTACTTCATTTTCTGAAAGTCTAGAGAATTACAACTTTGGTG 1833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute of Basic Medical Sciences: Tennodai 1-1-1, Tsukuba,
Ibaraki 305-8575, Japan (E-mail:hideyo-semd.tsukuba.ac.jp,
Tel:81-298-53-3282, Fax:81-298-53-3039)
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/protein_id="BAA82628.1"
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Tllrgvsiiigtiidagifispkgvlontgsvgmsltiutvgcylslegalsyaelgt
Tlkrgsghtytyilevpeplparvrwellitrpaatavislasertilepffigcei
Pelaiklitavsgityvmvysswsahjoiflifckltailiiivpgvwollkgop
Onfkoafsgrossitarlafyrgmyayagmfylnfytevenpertiplaicismai
VTIGYVLTNVAYFTTINAEELLISNAVAYFSERLLGNFSLAVPIFVALSCFGSMNGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cystine/glutamate exchanger: cDNA cloning and upregulation by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-APR-2000) Yoshikatsu Kanai, Kyorin University School of Medicine, Department of Pharmacocity and Toxicology; 6-20-2 Shinkawa, Mitaka, Tokyo 181-8611, Japan (E-mail: ykanaiekyorin-u.ac.jp, Tel:+81-422-47-5511(ex.3453),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                             1714 CCAGAAGAAGATAAGTTATGAACTAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGA 1773
1541 CTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1600
                                    1594 ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTATATGGGACAAGAAACCCAGG 1653
                                                                                                         1654 TGGTTTAGAATAATGTCAGAGAAAATAACCAGAACATTACAAATAATACTGGAAGTTGTA 1713
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                                                       1601 AFCACTCTGACTGGAGTCCCTGCGTATTATTATTATATATGGGACAAGAAACCCAGG
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Kim,J.Y., Chairoungdua,A., Cha,S.H., Segawa,H., Matsuo,H.,
Kim,D.K., Endou,H. and Kanai,Y.
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/protein_id="BAB40574.1"
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AB040875.1 GI:13516845
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Kanai, Y.
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SFARWLFIGLAVAGLIYLRYKCPDMHRPFKVPLFIPALFSFTCLFMVALSLYSDPFST
GIGFVITLIGVPAYYLFIIWDKKPRWFRIMSGFLALMPAQACDM"
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                                                                                                 59.8%; Score 1339;
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Matches 1339; Conservative
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PRI 30-MAR-2002
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Submitted (15-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                1201 TCCATGATTCATGTCCGCAAGCACACTCTTACCAGCTGTTATTGTTTTGCACCCTTTG 1260
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Homo sapiens BAC clone RP11-725C19 from 4, complete sequence.
AC110804
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Pearman,C., Kozlowicz,A. and Dignan,G.
The sequence of Homo sapiens BAC clone RP11-725C19
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Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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3 (bases 1 to 64196)
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Waterston, R. H.
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Mar 21, 2002 this sequence version replaced gi:19073866.
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                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 511-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
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Actual start of this clone is at base position 185268 of
RP11-393A12; actual end is at base position 64196 of RP11-725C19.
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                                                                                         Center: Washington University Genome Sequencing Center
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                                                                                                                    Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
                                                                                                                                                                                                                                                     Center project name: H_NH0725C19
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/rpt_family="AT_rich"
312. .607
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[1113. .1536
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2400, .2427
/rpt_family="AT_rich"
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/chromosome="4"
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3829. .4216
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3413. .3435
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1837. .4405
"note="similar to Bos taurus EST B1539797 (NID:g15380907)"
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4153. .4433
                                                                                                                                                                                                                   1933. .4394
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71244. .7125
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5074. :5447
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/note-"match to EST BG254117 (NID:912763933)"
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                                                                                                                                                                                                    'note="match to EST BI857800 (NID:g15998547)"
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6000. .6124
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/note="match to EST AW996897 (NID:98257131)"
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4233
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6899. .7362
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11395 TCTACAACATATGTTAGCACGGCAAAGAACCTTCAAATTGAAGACTGAGATTTTTCTGTA 11336
                                                                                                                                                                                                                                                                                                                                               11695 ATGAACTAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATT 11636
                                                                                                                                                                                                                                                                                                                                                                                                1731 ATGAACTAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATT 1790
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                                                                                                                                                                                                                                                                                                                              1671 AGAGAAAATAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAAGATAAGTT 1730
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                 7174. 7495
/note="match to EST BF927528 (NID:g12325656)"
7253. 7848
/note="similar to Homo sapiens EST BG499179
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7836. .8011
/rpt_amily="AcHobo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2031 TCTACAACATATGTTAGCACGGCAAAGAACCTTCAAATTGAAGACTGAGATTTTTCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 64196;
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/note="match to EST AW996897 (NID:g8257131)"
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                                                                                                                                                                                                                                                      21.4%; Score 479; DB 9; L
99.8%; Pred. No. 4.5e-261;
tive 0; Mismatches 1;
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Sequence 442 from Patent WO0172295.
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AX321911.1 GI:17906521
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Matches 529; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jiang,Y., Hepler,W.T., Clapper,J.D., Wang,A. and Secrist,H. Compositions and methods for the therapy and diagnosis of colon
                                                                                                                                                                                                                                                                    61 AGAATTAAGGAAAAAAGAAAGAAAGAAAAAAGAGAGAGGAAATTCCAGGCCAATTGTGG 120
                                                                                                                                                                                                                                                                                        121 CAFAGATTTTATCATATTCTGGATTTTTTGGATTCTTTTGTTTTCTCATCACTGGATTCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 ACCATCATTGGAGCAGGAATCTTCATCTCTCTAAGGGCGTGCTCCAGAACACGGGCAGC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 ACCATGATGGAGGAGGAATCTTCATCTCTCTAAGGGGGTGCTCCCAGAACACGGGCAGC 150
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                                                                                                                                                                                                    1 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAC 60
                                                                                                                                                                                                                         4 GGAGGTTGAAGTGAGCAGAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAC 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 AGGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGA 284
                                                                                                                                   Query Match 12.6%; Score 281; DB 6; Le Best Local Similarity 100.0%; Pred. No. 4.1e-148; Matches 281; Conservative 0; Mismatches 0;
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Pred. No. 2.9e-141;
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0; Mismatches
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CORIXA CORPORATION (US)
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AX351341
                                 1. .337
/organism="Homo sapiens"
/db_xref="taxon:9606"
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151 c 126 q 156
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Submitted (10-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA
4 (bases 1 to 161280)
Waterston, R. H.
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                                                                                                                                                                                                                                                       PRI 01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
514 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 573
                                            89 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 30
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Submitted (04-0CT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                               Homo sapiens BAC clone RP11-733C7 from 4, complete sequence. AC093903 AC055827 AC093903.3 GI:15920156
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Center code: WUGSC
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The sequence of Homo sapiens BAC clone RP11-733C7
Unpublished (2001)
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                                                                                          574 GAAGICITIGGICCATIACCAGCITITGI 602
                                                                                                                1 (bases 1 to 161280)
Sulston, J.E. and Waterston, R.
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5 (bases 1 to 161280)
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MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D.

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McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org SOURCE INFORMATION:

NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the right is RP11-310A13. Actual start of this clone is at base position 1 of RP11-733C7; actual end is at base position 161280 of RP11-733C7.

Data from AC009792 was used to finish the clone, AC055827

The sequence of AC055827 has been incorporated into AC093903 /134. ./385 /note="similar to EST BG989897 (NID:g14393967)" BG388107 (NID:913281553) 1866. .7318 "note="similar to EST C06175 (NID:g1502951)" /organism="Homo sapiens" 306. .406 //rpt_family="(GGAA)n" 471. .525 /rpt_family="AT_rich" 530. .782 /clone="RP11-733C7" /clone_lib="RPCI-11" 148. 334 /rpt_family="L1" 306. 406 7777. .7918 'note="similar to EST /rpt_family="L1"
5938. 5982
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6062. 6195. "Trpt_family="MIR"
6388. 6462 /db_xref="taxon:9606" /chromosome="4" rpt_family="GA-rich" 697. .1836 'rpt_family="AT_rich" /rpt_family="AT_rich" 8721. .9018 4295. .4325 /rpt_family="(A)n" 5625. .5960 Location/Qualifiers 1. .161280 /rpt_family="(TA)n" 1383. .1472 /rpt_family="MIR" 4013. .4321 /rpt_family="Alu" 4295. .4325 /rpt_family="L1" 1837. 1956 /rpt_family="L1" 6866. .7318 /rpt_family="L2" 5546. .6868 530. .782 /rpt_family="L1" /rpt_family="L1" 3005. .3221 repeat_region nisc_feature misc_feature misc_feature FEATURES

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17772. .18329

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/rpt_family="MER1_type"

20734. .20944
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12516. 12539
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hnote="similar to EST BG388107 (NID:g13281553)"
17329. .17618
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// Anote="similar to EST A1313891

17548. 17869

// Anote="similar to EST BF095483

17772. 18329
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1861. .11987
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.3275. .13304
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15823. 16117
/rpt_family="Alu"
17329. 17894
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3696. .13838
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2929. .13232
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0835. .10878
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3237. .13274
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4127. .14153
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2805, .22804
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2685. .22824
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10217. .10246
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Gaps ; 0 Length 161280; Indels 8.1%; Score 182; DB 9; 100.0%; Pred. No. 1.6e-91; live 0; Mismatches 0; Query Match Best Local Similarity 100.(Matches 182; Conservative

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repeat_region

Db 27756 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACACTGAGAGACTCTCTCAAAC 27697 1 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAC 60 δλ

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TLLRGVSIIIGTIIGAGIFISPKGVLQNTGSVGMSLTIWTVCGVLSLF"
1556. .>1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       27696 AGAATTAAGGAAAAAAGAAAGAAAGAAAAAAGAAAAGGAAATTCCAGGCCAATTGTGG 27637
                                                                                                  27636 CATAGATTTATCATATTCTGGATTTTTTGGATTCTTTTGTTTTCTCATCATGATTCA 27577
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                                                                               121 CATAGATTTTATCATATTCTGGATTTTTTGGATTCTTTTGTTTTCTCATCACTGGATTCA 180
61 AGAATTAAGGAAAAAAGAAAGAAAAAAAAGAGAGAGAGGAAATTCCAGGCCAATTGTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (24-APR-2000) Hideyo Sato, University of Tsukuba,
Institute of Basic Medical Sciences: Tennodai 1-1-1, Tsukuba,
Ibaraki 305-8575, Japan (E-mail:hideyo-s@md.tsukuba.ac.jp,
Tel:81-298-53-3282, Fax:81-298-53-3039)
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/protein_id="BAA94999.1"
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/db_xref="taxon:9606"
1001. .1683
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Submitted (29-MAY-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Apr 24, 2002 this sequence version replaced 9::20136935.
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Submitted (30-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (13-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3994)
Sulston,J.E. and Waterston,R.
                                                                                                                                         AC116610 3994 bp DNA linear PRI 29-Ni
Homo sapiens BAC clone RP13-562H2 from 4, complete sequence.
AC116610
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                      454 GIGGGCAIGTCICIGACCAICIGGACGGIGTGGGGGTCCTGTCACTATTTGG 506
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Contact: sapiens@watson.wustl.edu
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Genome Res. 8 (11), 1097-1108 (1998)
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3 (bases 1 to 3994)
Waterston, R.H.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

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Female blood DNA was isolated from one randomly chosen donor (out of 10 female blood DNA was isolated from one randomly chosen donors) and partially digested with a combination of EcoRI and EcoRI Methylase for library segments 12.2 or either MboI into the pBACe3.6 vector between the EcoRI sites for library segments 12 or the BamHI sites for library segments 12 or the BamHI sites for library segments 18.2 or the BamHI sites for library segments 344. The lightion products were transformed into DHIOB electrocompetent cells (BRL Life Technologies). The library has been arrayed into 384-well microtiter dishes and also gridded onto 22x2cm nylon high density filters for screening by probe hybridization.
                                                                                                                                                                                       The RPCI-13 Human Female BAC Library was constructed using improved cloning techniques developed by Kazutoyo Osoegawa. The library was generated by Bachui Zhao in our laboratory. Construction was funded by a grant from the National Human Genome Research Institute (NHGRI, NIH) (#IROIRGOlib5-03). The library was generated according to the new NHGRI/DOE 'Guidance on Human Subjects in Large-Scale DNA
                                            McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A single plasmid subclone region exists between bases 2382-2397. Polymorphisms have been identified between AC110804, AC093903, AC105310, and AC116610.
                                                                                                                                                                                                                                                                                                                                                                                                Female blood was obtained via a double-blind selection protocol
                       Mapping information for this clone was provided by Dr. John D.
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Pred. No. 9.5e-61;
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/db_xref="taxon:9606"
/chromosome="4"
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1606. 1716
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935. .1089
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2524. .2678
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2465. .2519
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/rpt_family="(TA)n"
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/rpt_family="L1"
2679. 2715
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/rpt_family="L2"
2142. .2299
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2300. .2400
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MAPPING INFORMATION:
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                                                                                                                                                                     SOURCE INFORMATION:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jiang,Y., Harlocker,S.L. and Secrist,H. Compositions and methods for the therapy and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 413
                                                                                        864 CTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCT 805
                                                                      TAACCTTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAA 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
749 CTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCT
                    Length 575;
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                                                                                                                                                                                                                                                                      linear
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Pred, No. 8.8e-49;
                                                                                                                                                                                                                                                                      DNA
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/db_xref="taxon:9606"
. 122 c 153 g 141
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

April 16, 2003, 10:51:38; Search time 3547 Seconds Run on:

(without alignments) 10223.201 Million cell updates/sec

....ttattaaaaaaaaaaaaa 2239 1 ggaggttgaagtgagcagag.. US-09-667-170A-440 2239 Perfect score: Sedneuce:

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

16154066 seqs, 8097743376 residues Searched:

0 Word size :

32308132 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

em_esthum:*
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em_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_fun:* em_gss_vrt:

dp_gss:*

em_estfun:* em_estom:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AL702210 DKFZp686C	AW205572 UI-H-BII-	BM887840 TMT023 Hu	BG490131 602519050	BG326527 602425373	BG284503 602408645
SUMMARIES	ID	9 AL702210	AW205572	BM887840	BG490131	BG326527	BG284503
	DB	. 6	10	14	12	12	12
	Query Match Length DB ID	516	483	511	919	910	936
d	Query Match	20.3	20.1	19.6	19.2	11.7	10.5
	Score	455	450	438	429	262	236
	Result No.	П	c 5	с 3	4	S	9

AQ002318 CIT-HSP-2 W00842 yz96d12.r1 AQ5336B1 RPCT-11-3 B3331 HS-1017-A1- BQ37058B PM0-GN034 BH860963 UP_336-3L BG388107 G02413070 BG186884 RST5861 A	BG186884 KS173861 A AW05922 LF1b04.yg AQ201392 RPCI11-60 AA812721 aj31y09.s AI102370 ES7211659 AI313891 hpi-7 PMA BE535700 601060361			AA922074 Gad7f09.x A1123247 Gad7f09.x BF095483 IL2-UT007 AA398455 £474708.s F737452 HSPD56219 H A1424212 £f63e10.x BQ013223 U1.1-BC1P BQ017470 U1.H-DT1-AA992074 ot37c10.s A1753931 cr16c05.x
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ALIGNMENTS

AL702210 516 bp mRNA linear EST 22-MAR-2002 DKFZp686C09156_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686C09156 5', mRNA sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 516) Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and AL702210 AL702210.1 GI:19685565 Wiemann, S.) Unpublished (1999) Contact: Bloecker H Homo sapiens human. MIPS LOCUS DEFINITION ORGANISM REFERENCE AUTHORS RESULT 1 AL702210 ACCESSION JOURNAL VERSION KEYWORDS SOURCE TITLE COMMENT

Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Bmail s.wiemannédkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.

No s1 sequence available. This clone (DKFZp686C09156) is available at the RZPD in Berlin.

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EST 02-DEC-1999
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 483)
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Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 bp mRNA linear EST 02-DEC-1
UI-H-BII-adt-h-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2718171 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                          /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1007 AAAACCCTGAAAAACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTG 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1067 GCTATGTGCTGACAAATGTGGCCTTACTTTACGACCATTAATGCTGAGGAGCTGCTGTT 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1127 CAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1187 CGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCAFGAACGGTGGTGTTTTGCTGTCTCCA 1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1367 TCTTCTCTGGAGACCTCGACAGICTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTA 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AAAACCCTGAAAAAACCCTTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCTTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 CGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTTGTCTCTCCA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 TCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGC 421
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Pred. No. 6.1e-125;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                              /organism="Homo sapiens"
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/clone_lib="686 (synonym: hlcc3)"
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/dev_stage="adult"
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oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
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Pred. No. 1.9e-123;
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                                                                                                                                                   I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward
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/clone="IMAGE:2718171"
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/note="Vector: pcDNA3; Site_1: EcoRI; Site_2: EcoRI; Human cdNA library made from mRNA isolated from trabecular meshwork cells established fom eyes from 6 individuals, ages 2 weeks to 2 years. Cells were harvested at passages 3 through 6. Invitrogen made a unidirectional cDNA library from the mRNA from the frozen cells using a pcDNA3 vector and TPO10F', host cells."
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1 (bases 1 to 511)
Wirtz,M.K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.
Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1636 TGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACCAGAACATTACAA 1695
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1634 TATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACCAGAACATTAC 1693
                                                                                                                                                                          1754 TGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATTTTTACTTCATTTTCTGAAAGTCT 1813
                     159 AAATAATACTGGAAGTTGTACCAGAAGAAGATAAGTTATGAACTAATGGACTTGAGATCT 100
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/clone_lib="Human Trabecular Meshwork cDNA library"
                                                                                      1694 AAATAATACTGGAAGTTGTACCAGAAGAAGAAGTTATGAACTAATGGACTTGAGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-4698
Fax: 503-494-6875
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/dev_stage="2 week to 2 year old infants"
/lab_host="TOPlOF'"
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Glaucoma Genetics Lab
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BG490131 919 bp mRNA linear EST 27-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 919)
                                                                                       1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2056 AGAACCTTCAAATTGAAGACTGAGATTTTTCTGTATATATGGGTTTTGTAAAGATGGTTT 2115
1756 GCAATCTGCCCAAGGGGAGACACAAAATAGGGATTTTTACTTCATTTTCTGAAAGTCTAG 1815
                                                                                                                                                                            1876 ATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATGTAGTTATAGAAAGTGAAT 1935
                                                                                                                                                                                                                                                                     1996 GGAGAAAAGACTAGACAATTACTATGTGGTCATTCTCTACAACATATGTTAGCACGGCAA 2055
                                                                                                                                                                                                   271 ATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATGTAGTAATAGAAAGGGAAT 212
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                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                    91 AGAACCTTCAAATTGAAGACTGAGATTTTTCTGTATATATGGGTTTTGTAAAGATGGTTT 32
                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1398 row: c column: 14
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/clone_lib="NH_MGC_18"
/tissue_type="large cell carcinoma"
/lab_host="PH108 (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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BG490131
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NIH_MGC Library.

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                            1404 CAGITITGCCAGGIGGCITITITATIGGCCIGGCAGITGCIGGGCTGATITATCTICGATA 1463
                                                                                                                                                                                                          CAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTC 1523
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                                                                                                                                                                                                                                                                                                                     1584 TGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTTATTATGGGACAA 1643
                                                                                                                                                                                                                                                                                                                                                                           1644 GAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAACCAGAACATTACAAATACT 1703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bG34b577 11near EST 27-FEB-60242373F1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:4562994 5'
                                                                                                                                                                  417 CAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTC 476
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                                                                     Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1276 row: b column: 19
High quality sequence stop: 706.
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0
                                            Length 919;
                                                                    Indels
                                       19.2%; Score 429; DB 12; I
100.0%; Pred. No. 1.8e-117;
ive 0; Mismatches 0;
 272
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/db_xref="taxon:9606"
/clone="IMAGE:4562994"
/clone_lib="NIH_MGC_14"
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Contact: Robert Strausberg, Ph.D. Email: Gappbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
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BG326527.1 GI:13132964
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                                         Query Match 19.2
Best Local Similarity 100.
Matches 429; Conservative
 195
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/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Corgan: Kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II.RT (Life Technologies)."
178 c 249 g 246 t
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
National institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAMI0463 row: 1 column: 11
High quality sequence stop: 795.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 ACCATCATTGGAGCAGGAATCTTCATCTTCTTCTAAGGGCGTGCTCCAGAACACGGGCAGC 453
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                                                                                                                                                                                                                                                                                                                                                                                                           11.7%; Score 262; DB 12; Length 910; 99.7%; Pred. No. 3.8e-68; ive 0; Mismatches 0; Indels
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                                                                                                                                          /note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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CIT-HSP-2283E8.TF CIT-HSP Homo sapiens genomic clone 2283E8, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: meddamsetigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13-21;
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     334 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 393
                                                                                                                                                                                                                                                                                                                                                                                   454 GIGGGCATGTCTCTGACCATCTGGACGGTGTGGGGGTCCTGTCACTATTTGGAGCTTTG 513
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                                                                  /clone="IMAGE:4537810"
/clone_lib="NHH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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                             /organism="Homo sapiens"
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/db_xref="GDB:7147907"
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                                                    /db_xref="taxon:9606"
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Unpublished (1998)
Other_GSSs: CIT-HSP-2283E8.TR
Location/Qualifiers
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(basa 1 to 371)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Riffin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, T.R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 4800
Email: est@Matson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                     335 AGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGCA 394
                                                                                                                                                                                                                                                                                       395 CCATCATTGGAGCAGGAATCTTCATCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCG 454
                                                                                                                                                                                                                                                                                                                                                                                  218 CCATCATTGGAGCAGGAATCTTCATCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCG 159
                                                                                                                                                                                                                                    Gaps
                                                                      /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/db_xref="GDB:3884033"
/db_xref="taxon:9606"
/clone="IMAGE:290903"
/clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                              2.2e-41;
                                                                                                                                                                                              Score 172; DB 17;
                                                                                                                                                                              7.7%; Sco. 100.0%; Pred. No. ... 0; Mismatches
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High quality sequence stop: 339.
/db_xref="taxon:9606"
/clone="2283E8"
                                    /clone_lib="CIT-HSP"
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1.371
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                                                          /sex="Male"
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/clone="RPCI-11-384K17"
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Best Local Similarity
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KEYWORDS
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Lones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://Dacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resega.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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  (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino." 50 c 69 g 115 t 6 others
                                                                                                                                                                                                                        1661 GAATAATGTCAGAGAAAATAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAG 1720
                                                                                                                                                                                                                                                                                                            1721 AAGATAAGTTATGAACTAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAA 1780
                                                                                                                                                                                                                                                                                                                                                                                                   1781 AATAGGGATTTTTACTTCATTTTCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAAACA 1840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AAGATAAGTTATGAACTAATGGNCTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAA 120
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                                                                                                                                                                                 Gaps
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                    Score 171; DB 14;
Pred. No. 6.2e-41;
0; Mismatches 3;
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/db_xref="GDB:7647328"
/db_xref="taxon:9606"
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LOCUS

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B33331 486 bp DNA linear GSS 17-OCT-1997 HS-1017-Al-G10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 792 Col=19 Row=M, DNA sequence.
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I (bases 1 to 486)
Mahairas, G. G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
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/cell_type="Lymphocytes"
/note="Yector: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Yector: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
72 q 140 t 1 others
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/clone="plate=CT 792 Col=19 Row=M"
/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"
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                                                                                                                                                                                                            Length 400;
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100.0%; Pred. No. 1.2e-35;
trive 0; Mismatches 0;
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Contact: Mahairas GG, Zackrone KD, Hood in the contact: Mahairas GG, Zackrone KD, Hood in the contact: Mashington Seattle, WA 98195, USA
Tel: (206) 685-7301
Email: kzackron@u.washington.edu
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Sequence Tagged Connector
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/clone_lib="RPCI-11"
/sex="Male"
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Class: BAC ends
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GSS 18-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheung, V.G., Dalrymple, H.L., Narasimhan, S., Watts, J., Schuler, G., Raap, A.K., Morley, M. and Bruzel, A. A resource of mapped human bacterial artificial chromosome clones Genome Res. 9 (10), 989-993 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 485)
                                                                                                                                                                                                               485 bp DNA linear GSS 18-JUL-20
UP_336-3L_SP6 RPCIII Human Male BAC Library Homo sapiens genomic
clone 336-3L, DNA sequence.
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/note="Vector: pBACe3.6; RPCI11 Human Male BAC Library"
197 c 93 g 163 t
             249 CTGTAGTGATGCTCCTAAATAGCATGAGTGAGCTGGAGCGCCCGGATCCAGATTTCT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        749 CTGTAGTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCT 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Pediatrics
University of Pennsylvania
3516 Civic Center Blvd, ARC 516, Philadelphia, PA 19104, USA
Fat: 215 590 3709
Email: sandya2@mail.med.upenn.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Narasimhan SL, Morley M, Burdick J, Cheung VG
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100.0%; Pred. No. 2.5e-28;
Live 0; Mismatches 0;
                                                                            1330 GCTGTTATTGTTTTGCACCCTTTGACAATGAT 1361
                                                                                                   266 GCTGTTATTGTTTGCACCCTTTGACAATGAT 297
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/db_xref="taxon:9606"
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Seg primer: SP6
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, F.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
271200-001-f12&t3=2000-12-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 106
High quality sequence stop: 117.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                         1210 TTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCCAGGTTATTCTATGTTGCGTCTCGA 1269
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62 GCACCCTTTGACAATGATAATGCTCTTCTGGAGACCTCGACAGTCTTTTGAATTTCCT 121
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 2e-35;
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Best Local Similarity 100.0%; Pred. No. 2e-
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/db_xref="taxon:9606"
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Email: scain@athersys.com
Fax: 216 361 9596
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Nat. Biotechnol. 19 (5), 440-445 (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1072)
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RST5861 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
BG186884
                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10421 row: k column: 17
High quality sequence stop: 625.
Location/Qualifiers
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                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nih.gov
Itsuse Procurement: Affor
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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100.0%; Pred. No. 6.7e-24;
tive 0; Mismatches 0; Indels 0;
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Tel: 216 431 9900
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/db_xref="taxon:9606"
/clone="IMAGE:4521736"
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Matches 112; Conserva
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                                                                                         REFERENCE
                                                                                                                AUTHORS
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bunaanila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 87)
Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
Burcham,T. and Albrecht,G.
In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
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/db_xref="taxon:9906"

/db_xref="taxon:9906"

/colne_lib="Athersys RAGE Library"

/coll_line="FH1080"

/note="See 'Creation of Genome-wide Protein Expression

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/cell_tipe="THP-1 (TIB-202)"
/note="Vector: pCR2.1; Cloning of PCR products from micro-beads carrying 3' end of up-regulated cDNA. THP-1 cells induced with 100 nM PMA in DMSO. "
1 9 c 14 g 27 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 CCTATTGGGGTTAGGAGAAAAGACTAGACAATTACTATGTGGGTCATTCTCTAACAAAT 219
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Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the up-regulated gate.
High quality sequence stop: 87.
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LF1b04.yg UPC15 Homo sapiens CDNA, mRNA sequence.
AW059922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2043 GITAGCACGCCAAAGAACCTICAAATIGAAGACIGAGATITT 2084
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100.0%; Pred. No. 8.2e-21;
tive 0; Mismatches 0;
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/clone_lib="UPC15"
High quality sequence stop: 441.
Location/Qualifiers
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us-09-667-170a-440.oli.rst

0; 0; Gaps Best Local Similarity 100.0%; Pred. No. 1.4e-15; Matches 87; Conservative 0; Mismatches 0; Indels

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Search completed: April 16, 2003, 14:10:03 Job time: 3558 secs

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Sequence 16, Appl
Sequence 7, Appl
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Sequence 10, Appl
Sequence 10, Appl
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                                                                April 16, 2003, 06:13:54; Search time 93 Seconds (without alignments) 7383.325 Million cell updates/sec
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Sequence 3, Appli
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                                                                                                                                        Sequence 75,
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6: /cgn2_6/ptodata/1/ina/pcyt/3_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-800-960-3
US-09-128-155-16
US-08-213-419B-3
US-08-77-223-7
US-09-370-838-166
US-09-780-049-18
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US-09-345-882-1
US-09-851-896-3
US-09-268-992-7
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PCT-US95-07201-43
US-09-875-223-2
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US-08-965-729A-2
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US-09-461-697-75
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US-09-033-556-3
US-09-268-992-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           nucleic search, using sw model
                                                                                                                                                               IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                   Issued_Patents_NA:*
                                                                                                                  US-09-667-170A-440
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Maximum DB seq length: 200000000
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Match Length DB
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99500
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152331
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Sequence Sequence

Sequence

Sequence

US-09-813-133A-3

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Sequence 4, Appli
Sequence 7, Appli
Sequence 401, App
Sequence 45, Appl
Sequence 1, Appli
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Sequence 1
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Sequence 3
Sequence 3
Sequence 3
Sequence 6
Sequence 6
Sequence 6
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Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
NUMBER OF SEQUENCES: 3
                                      US-09-281-4818-18
US-09-784-673-3
US-09-774-673-3
US-09-774-673-3
US-09-774-673-3
US-09-71-211-3
US-09-146-053-6
US-08-680-395-6
US-08-680-395-6
US-08-681-527-19
US-08-520-373D-4
US-09-641-678-401
                             US-09-018-584A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,362
                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF-0514 US
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Patent No. 5942399
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CELTONE, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PP-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer
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54.6%;
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COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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LENGTH: 2072 base pairs
471
81001
6405
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87543
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ADDRESSEE: Incyte Ph
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Best Local Similarity
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LIBRARY: ESOGTU
CLONE: 2667831
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US-09-073-362-2
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1140 AGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGC 1199
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                                     300 CGCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAAAAGTGCAGCTGAAGAAGT 359
                                                                                                              360 CACTITACIGAGGGGAGICICCATIAICATIGGCACCAICATIGGAGCAGGAAICTICAI 419
                                                                                                                                  420 CICICCIAAGGGCGIGCICCAGAACACGGGCAGCGIGGGCAIGICICIGACCAICIGGAC 479
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                                                                                                                                                                                                                                                                                    600 TGTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCT 659
                                                                         192 CICCCCTITGGGIGATGGGGCCAGCCCAGGCCGGAGCAGGIGAAGCTGAAGAAGGAGAT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                        780 CAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGAT
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 0; Mismatches 606; Indels
   Matches 730; Conservative
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1380 CCTCGACAGICTTITGAATTICCTCAGTTTIGCCAGGTGGCTTTTTATTGGGCTGGCAGT 1439
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                          1440 IGCTGGGCTGAITTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCC 1499
                                                                                                                          1392 CGTTTTCTTCCCGATTGTCTTCTGCCTCTGCACCATCTTCCTGGTGGCTGTTCCACTTTA 1451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastsEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/243,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF-0514 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/073,362
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09243920 Patent No. 5981242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
                                                                                                                                                                                                                                                                                                                                                                            1620 TTATCTCTTTATTATA 1635
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 650-855-055
TELEFAX: 650-845-4166
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STRANDEDNESS: single
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LIBRARY: ESCC.
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GTGCAGCTGAAGAGGAAAGT 359 [11	GCTGAATTGGGAACAACTAT 539	GCTACTGCTGATATCCCT 659	GTCCTAAATAGCATGAGTGT 779	89	GCTTTTTATTATGGAATGTA 959	10	CTGCTTTCAAATGCAGTGGC 1139 	GCAGTTCCGATCTTTGTTGC 1199 ATAATTCCACTGTCAGTTGC 1091	GTCTCCAGGTTATTCTATGT 1259 	ATTCATGTCCGCAAGCACAC 1319 	ATATGCTCTTCTGGAGA 1379
CGCCTTTCAGGAAGAGCGCCTTTCAGGAAGAGAAAGTGCAGCTGAAGAGGAAAGT				AATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCGGTATTATAAGGTCGATAGTTGTTAAAGACGCGGGGGGCCTCTACTTTGAGAATTCGTTAGAATTTGAGAATTCGATTGGTAAGAATTCGAGGAGCCTCTACTAGTTTTGAGAATTC	CTTTCAGGAAGAGTTCAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTA	AACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGAC	AAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTGCTTTCAAATGCAGTGG 	AGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGCTGC 	CCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGT	TGCGTCTCGAGAGGGTCACCTTCCAGAATCCTCTCCATGATTCATGTCCGCAAGCACAC 	TCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGA
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1560 TTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTTGACTGGAGTCCCTGCGTA 1619
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                    1440 TGCTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCGTCTTTCAAGGTGCC 1499
                                                                                         1500 ACTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTA 1559
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TILE OF INVENTION: HUMAN TUMOR-ASSOCIATED MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.4%; Score 211.4; DB 2; Length Best Local Similarity 56.3%; Pred. No. 2.8e-49; Matches 395; Conservative 0; Mismatches 306; Indels
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SOFTWARE: FSASLENG for Windows Version 2.0
CURTENY APPLICATION DATA:
APPLICATION NUMBER: US/08/825,781
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF-0262 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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US-08-825-781-2
; Sequence 2, Application US/08825781
; Patent No. 5843727
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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| IMMEDIATE SOURCE:
| LIBRARY: PANCTUTO2
| GLONE: 2236771
| US-08-825-781-2
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COUNTRY: U
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1055 TTGTCACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAGG 1114
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                                                    CTGAAGAAGTAGAAAACCCTGAAAAAACCATTCCCCTTGCAATATGTATATCCATGGCCA 1054
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COUNTRY: USA
ZIP: 22313-0299
ZIP: EADPALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPA:
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PatentIn Release #1.0, Version #1.25
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Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
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STATE: VA
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GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOI158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.0%; Score 67.4; DB 1;
Best Local Similarity 2.1%; Pred. No. 1.3e-08;
Matches 8; Conservative 235; Mismatches 136;
                                                                                                                                                                              TELECOMMUNICATION NOMES: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELERAX: (703)883-4109
TELERAX: (703)883-4109
TELEX: 899149
INFORMATION POR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTONNEY, AGGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/800,960 CURRENT FILING DATE: 2001-03-08 NUMBER OF SEQ ID NOS: 4
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US-09-800-960-3/c
; Sequence 3, Application US/09800960
; Patent No. 6387677
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US-08-757-223-7
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TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: J11.002CNCP
CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR APPLICATION NUMBER: US 07/870,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 151204 GGAGGTTGCAGTGAGGAGATCGTGCCACTGCACTCCAGCTGGGTGACAGGGAGACTC 151263
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: ANOUEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                      23 CATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAACAGAATTAAGGAAAAAAAGA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels 10; Gaps
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Pred. No. 0.0011;
0; Mismatches 29; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                    Db 43539 AAGCAATCTTTTAAGATATCATTATAGGCCAGGCGTGG 43502
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2.2%; Score 50; DB 3;
Best Local Similarity 73.2%; Pred. No. 0.005;
Matches 82; Conservative 0; Mismatches 2
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Patent No. 6117654
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                                         NAME/KEY: misc_feature

LCCATION: (1)...(62804)

; OTHER INFORMATION: n = A,T,C or G

US-09-800-960-3
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; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
                                                                                                                                                                       2.3%;
                                                                                                                                                                                              Best Local Similarity 70.49
Matches 69; Conservative
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APPLICANT: Inselbu
ORGANISM: Human
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                                                                                                                                                                         Query Match
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2350 AIGTITGATITATITATITITITITITATGITATAATATATGTATITATAATATATA 2291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Poduslo, Shirley E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ASSESSING RISK
TITLE OF INVENTION: FACTORS IN ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 2.0%; Score 44.8; DB 4; Length 6124; Best Local Similarity 53.4%; Pred. No. 0.024; Matches 94; Conservative 0; Mismatches 82; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,223
FILING DATE: No. 6136530ember 27, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Locke Purnell Rain Harrell
STREET: 2200 Ross Avenue, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REFERENCE/DOCKET NUMBER: 4-003US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08757223
Patent No. 6136530
                                                                                                            TYPE: DNA ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 214/740-8785
1992-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                   NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               94; Conservative
                                                                                                                                                                                                 (2407) . . (2439)
CDS
(2598) . . (3404)
CDS
(3580) . . (3720)
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STRANDEDNESS: single
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ZIP: 75201-6776
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (3850)..(5835)
US-08-213-419B-3
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                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (240
NAME/KEY: CDS
                                                                                       6124
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US-08-757-223-7
                                                                                                                                                                                                                                                    LOCATION:
NAME/KEY:
                                                              SEQ ID NO 3
                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                        FEATURE
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APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
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Pred. No. 0.36;
0; Mismatches 15; Indels
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APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTIENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
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LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base
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CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR PILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/798,096 CURRENT FILING DATE: 201-03-01 NUMBER OF SEQ ID NOS: 89
                                                                                                                                        7064 AAGCCCACAAAAACAAAATCTTCC 7040
                                                                                                   83 AAGAAAAAGAGAGAGGAAATTCC 107
                                                                                                                                                                                                                                          Sequence 10, Application US/09798096 Patent No. 6399378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09345882 Patent No. 6399373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.9%;
Best Local Similarity 77.6%;
Matches 52; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: 5-124-273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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LOCATION: 72794
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US-09-798-096-10/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 99500
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US-09-798-096-10
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Patent No. 646520

GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: EXPRESSION
FILLE OF INVENTION: EXPRESSION
FILLE OF INVENTION: EXPRESSION
FILLE NET FRENCE: US/09/780,049
CURRENT FILLING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 96
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                                                                                                       2550 GGGAGTTACAGTGGCCAACATTGTGCCAGCCTGGGTGACAGAAGGAGACTCTGTCTCAA 2609
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                                                                                  1 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 AGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAACAGAATTAAGGAAA 73
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1.9%; Score 43.6; DB 3; Length 5375; 67.8%; Pred. No. 0.049; clive 0; Mismatches 29; Indels 0
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NGC, MIChael J.
APPLICANT: NGC, MIChael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFREENT APPLICATION NUMBER: US/09/370,838
CURRENT APLICATION NUMBER: US/09/370,838
FARLIER APPLICATION NUMBER: US/09/285,323
NUMBER OF SEQ ID NOS: 289
SEQ ID NOS: 289
SEQ ID NOS: 289
LENGTH: 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.9%; Score 43.4; DB 4; Length 893; Similarity 62.4%; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AAAGAAAGAAAAAAAAGAGAGAGAGAAATTCCAGGCCAATTGTGGCA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                    61 AGAATTAAGGAAAAAAAAAA 90
                                                                                                                                                                                                                                                                                                    Sequence 166, Application US/09370838; Patent No. 644425; Patent No. 644428; ADENEAL INFORMATION: APPLICANT: Reed, Steven G.
                                           61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapien
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 59; Conserv
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US-09-780-049-18/c
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      Query Match
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                          Best Local
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Matches
                                           Matches
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US-09-864-761-48172

Length: 34
Matches: 8
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0 Alignment Scores:
Pred. No.:
Score:
Score:
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Ouery Match: 1.09%
DB:

US-09-667-170A-440 (1-2239) x US-09-864-761-48172 (1-34)

Search completed: April 16, 2003, 16:57:06 Job time: 48 secs

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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MAP TO AL118523.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
                                                                                                                                                                                                                                                            US-09-667-170A-440 (1-2239) x US-09-864-761-41510 (1-34)
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                  34
                                                                                      Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLILNG DATE: 2000-09-21
PRIOR PLILNG DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLILNG DATE: 2000-09-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLILNG DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                        Matches:
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PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE:
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 48172, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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100.00%
1.09%
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                                                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-864-761-48172
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                                                                                                     Percent Similarity:
Alignment Scores:
Pred. No.:
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                                                                               Score:
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9

US-09-864-761-41510
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF LINGARIAN.

TURE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-06-36

PRIOR PILING DATE: 2000-06-36

PRIOR PILING DATE: 2000-01-03

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-09
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OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR PILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 09/608,408
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                                                    Sequence 41510, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                 US-09-864-761-41510
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LENGTH: 34
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                                          Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                               STATEMENT AND STATEMENT OF THE CONTROLL AND STATEMENT OF TATLE OF INVENTION: 36 Human Secreted Proteins of TILE REPERENCE: 920291
CURRENT APPLICATION NUMBER: US/09/739, 907
CURRENT FILING DATE: 2000-12-20
PRIOR FILICATION NUMBER: 09/348,457
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1998-01-07
PRIOR PRIOR PRICATION NUMBER: 60/070,652
PRIOR FILING DATE: 1998-01-07
SOFTWARE FOR DID NOS: 196
SSOFTWARE: PATCHTION NUMBER: 60/070,658
NUMBER OF SEQ ID NOS: 196
SSOFTWARE: PATCHTION OF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: 36 Human Secreted Proteins
                          Matches:
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Matches:
        ength:
                                                                                                   Gaps:
                                                                                                                                                                 409 GGAATCTTCATCTCCTAAGGGCGTGCTC 438
                                                                                                                                                                                    57 GlyllePhelleSerProLysGlyValLeu 66
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CURRENT APPLICATION NUMBER: US/09/739,907
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/348,457
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 87, Application US/09739907
Patent No. US20010012889A1
GENERAL INFORMATION:
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                          Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                          RESULT 11
US-09-739-907-99
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Pred. No.:
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LOCATION: (170)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.

TITLE OF INVENTION: 36 Human Secreted Proteins
FILE REFERENCE: PSO22A1

CURRENT APPLICATION NUMBER: US/09/739, 907

CURRENT FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 09/348, 457

PRIOR APPLICATION NUMBER: 60/070, 567

PRIOR FILING DATE: 1998-01-07

PRIOR FILING DATE: 1998-01-07

PRIOR FILING DATE: 1998-01-07

PRIOR APPLICATION NUMBER: 60/070, 704

PRIOR FILING DATE: 1998-01-07

NUMBER OF SEQ ID NOS: 196
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Mismatches:
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PRIOR APPLICATION NUMBER: 60/070,692
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR APPLICATION NUMBER: 60/070,658
NUMBER OF SEQ ID NOS: 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QY 1993 TTAGGAGAAAAGACTAGACAATTACTA 2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 191, Application US/09739907
; Patent No. US20010012889A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                 NAME/KEY: SITE
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LOCATION: (180)
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LENGTH: 182
                                                                                                                                                                                          TYPE: PRT
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US-09-667-170A-440 (1-2239) x US-09-739-907-191 (1-182)

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Sequence 16, Application US/09815923
Sequence 16, Application US/09815923
Sequence 16, Application No US20020197644A1
Sequence 16, Application No US20020197644A1
SENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of Insect Call Membrane Transporters as No. US20020197644A
TITLE OF INVENTION: Use of Insect Call Membrane Transporters as No. US20020197644A
TITLE OF INVENTION: Target Sites for Insecticides
FILE REFERENCE: 023070-033800US
CURRENT PALLING DATE: 2001-03-23
NUMBER OF SEC ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-080C
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US-09-667-170A-440 (1-2239) x US-10-163-866-42 (1-511)
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Conservative:
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                                           517 TATGCTGAATTGGGAACAACTATAAAGAAATCTGGA 552
                                                                  CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT APPLICATION NUMBER: US/02/06.05
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR PPLICATION NUMBER: US 60/328,605
PRIOR PLING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR FILING DATE: 2001-10-2
PRIOR PLING DATE: 2001-10-2
PRIOR PLING DATE: 2002-02-15
PRIOR PLING DATE: 2002-02-15
PRIOR PRILING DATE: 2002-02-15
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Best Local Similarity:
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FILE REFERENCE: EX02-080C
FILE REFERENCE: EX02-080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT APPLICATION NUMBER: US/02/96,076
PRIOR FILING DATE: 2002-06-05
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-12
PRIOR PLICATION NUMBER: US 60/338,733
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR PLICATION NUMBER: US 60/357,253
PRIOR PLICATION NUMBER: US 60/357,600
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-03-15
                           TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE PILE REFERENCE: EX02-080C CURRENT APPLICATION NUMBER: US/10/163,866 CURRENT FILING DATE: 2002-06-05
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Score: 10.00
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Best Local Similarity:
      GENERAL INFORMATION:
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62 GAATTAAGGAAAAAAAAAAAAAAAAAGAGAGAAAATTCCAGGCCAATTGTGGC 121
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APPLICANT: Benson, Darin R.
APPLICANT: Blliot, Mark
APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
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APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
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Mismatches:
Indels:
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Matches:
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CURRENT APPLICATION NUMBER: US/09/738,973
UNMBER OF SEQ ID NOS: 587
                 Sequence 586, Application US/09738973
Patent No. US20020110563A1
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                                                                 Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
                                                                                                                             Mohamath, Raodoh
                                                                                                                                            Algate, Paul A.
Secrist, Heather
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US-09-738-973-586
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US-09-738-973-586
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LENGTH: 97
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APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Algate, Paul A.
APPLICANT: Serist, Heather
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Elliot, Mark
APPLICANT: Elliot, Mark
APPLICANT: Ranion, Jane
APPLICANT: Ranion, Jane
APPLICANT: Ralos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                               104 TTCCAGGCCAATTGTGGCATAGATTTTATCATATTCTGGATTTTTTGG 151
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FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: PRASTSEQ for Windows Version 3.0
SEQ ID NO 587
LENGTH: 16
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CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
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; Publication No. US20030027188A1
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Henderson, Robert A.
Lodes, Michael J.
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ORGANISM: Homo sapiens
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Query Match:
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US-10-163-866-41
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36 GluLysValGlnLeuLysArgLysValThrLeuLeuArgGlyValSerIleIleIleGly 55
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              21 GluLeuargLysLysGluArgLysLysLysLysRygluArgLysPheGlnAlaAsnCysGLy 40
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILLE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEO ID NOS: 735
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Mismatches:
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                                                                                                                                                                                                                                                                                    Sequence 586, Application US/09854133 Publication No. US20020183499A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
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501 466 0 0 0	1) GTCTCCATTATC? 	CCAGAACACG	CACTATTGGA erLeuPheGly	ATTACACAT isTyrThrT	CAT	PACATTCTGGAACCAT	TGGGCA alGlyI	CAGATI	ATGCAG MetGln	CAAGTATTACGC 	TTTACCTCAACTTTC 	TATCC	TTAATG 	CTACTGGG LeuLeuGl	CCATGAACGGTGG 	
Length: Matches: Conservative: Mismatches: Gaps:	3-866-48 (1-50) ACTTTACTGAGGGAC	GGGCGTG	GTGTGGGGTCCTGT 	AAATCTGGAGGTC LysSerGlyGlyH	TACGAGTCTGGGTGG 	3CATTTGGACGCTACA 	TCATTA euileī	TGGAGCGCCCGGATC 	ATAGTCCCTGGAGTT 	TTTCAGGAAGAGATT 	SCATATGCTGGCTGGT: 	ATTCCCCTTGCAATATGTA 	GCCTAC	ACCTTTTCTGAGCGC ThrPheSerGluArg	CCTGCTTTGGCT 	CTCGAGAGGGTC
66.00 00.00% 00.00% 3.66%	(239) x US-10-163 TGAAGAGAAAGTCAC'	TTCATCT 	CATCTGGACGGT rileTrpThrVa	GAACAACTATAAAGI yThrThrIleLysI	TTACCAGCTTTTGTF LeuProAlaPheVal	FGATATCCCTG(CTGAACTTGCGATCAAGC 	SCATGAGTGTCAGCT(CAATTCTGATAATT 	TTAAAGACGCCTTT 	PATTATGGAATGTATGCA 	AGAAAACCCTGAAAAAACCAT 	TGTGCTGACAAATGTG rValLeuThrAsnVal	CAGTGGCAGTG 	CTTTGTTGCCCTCT 	TTATTCTATGTTGCGTC
cores: 0 4 4 1larity: 1 31milarity: 6	170A-440 (1-2239) GAGAAAGTGCAGCTG/ 	ACCATCATTGGAGCAC 	3TGGGCATGTCTCTGAC	CTTATGCTGAATTGG 	AAGTCTTTGGTCCA 	CTGCAGCTACTGCTGT 	ATTCAATGTGAAATCC 	GTGATGGTCCTAAATAGCA 	TTTGCAAGCTCACAG	GTCAAACGCAGAACTTTAAAGACGCCT 	ACTGGCTTTT 	CTGAAGAAGTAGAAA 	TTGTCACCATTGGCTATC	AGCTGCTTTCAAATG 	CATTAGCAGTTCCGAT	TGCTGTCTCCAGG
gnment d. No.: re: cent Si t Local ry Matcl	334	394 #	454 G 16 V	514 T 96 S	574 G 1 116 G	634 C	694 A 156 I	754 G 176 V	814 T	874 G	934 CC. 236 Pro	994 A(256 T	1054 AT	1114 GP 1 296 G1	1174 TC 316 Se	1234 TT 336 Ph
Alip Pre- Sco Per- Bes- Que- DB:	US- Qy Db	oy Op	Oy Dp	Qy	Qy Db	Oy Dp	Qy Dp	Oy Dp	Oy Dp	Qy Dp	Qy Dp	Oy Dp	Qy	Oy Dp	Qy Db	Oy Dp

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US-10-153-866.49

Sequence 49, Application US/10163866

Sequence 49, Application US/10163866

PUBLication No. US20030027188A1

GENERAL INFORMATION:

APPLICANT: EXELIXIS, INC.

TILE OF INVENTION: SLC75 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

FILE REFERENCE: EX02-080C

CURRENT FILING DATE: 2002-06-05

PRIOR APPLICATION NUMBER: US 60/296,076

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2002-02-15

PRIOR FILING DATE: 2002-02-15

PRIOR APPLICATION NUMBER: US 60/3357,600

PRIOR FILING DATE: 2002-02-15

PRIOR APPLICATION NUMBER: US 60/357,600
1354 ACAATGATAATGCTCTTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCC 1413
                                                                                                                       1414 AGGTGCCTTTTTATTGGCCTGGCAGTTGCTGGCTGATTTATCTTCGATACAAATGCCCA 1473
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SOFTWARE: Patentin version 3.1
SEQ ID NO 49
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US-10-163-866-48
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LENGTH: 501
TYPE: PRT
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-Q=/CGR12_1/USPTQ_spool/US09667170/runat_04042003_091003_21265/app_query.fasta_1.2375
-Q=/CGR12_1/USPTQ_spool/US09667170/runat_04042003_091003_21265/app_query.fasta_1.2375
-D=Published_Applications_AA -OFMT=fastan -SUFFTX=0.01ap_rapb -MINNATCH=0.1
-LOOPCEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=0.1go
-LOOPCET=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=0.1go
-ALIGN=1S -MODE-LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=0205967170_eCGN_1_LIS_druat_04042003_091003_21265
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEGUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEDUT=120 -WARN_TIMEOUT=80 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Sequence 586, App
Sequence 586, App
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Sequence 49, Appl
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8061.880 Million cell updates/sec
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                                                                                                                                                                                                            Description
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2: Cggn2_6/ptodata/1/pubpaa/PCT_NBW_PUB.pep:*
3: Cggn2_6/ptodata/1/pubpaa/USOB_NBW_PUB.pep:*
4: Cggn2_6/ptodata/1/pubpaa/USOF_NBW_PUB.pep:*
5: Cggn2_6/ptodata/1/pubpaa/USOF_NBW_PUB.pep:*
6: Cggn2_6/ptodata/1/pubpaa/USOF_NBW_PUB.pep:*
7: Cggn2_6/ptodata/1/pubpaa/USOF_NBW_PUB.pep:*
8: Cggn2_6/ptodata/1/pubpaa/USOB_NBW_PUB.pep:*
9: Cggn2_6/ptodata/1/pubpaa/USOB_NBW_PUB.pep:*
10: Cggn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
11: Cggn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
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13: Cggn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
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14: Cggn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
                                                                                                                April 16, 2003, 16:40:19 ; Search time 42 Seconds
                    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                  - protein search, using frame_plus_n2p model
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US-10-163-866-49
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US-09-738-973-586
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60.0 , Ygapext 60.0
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Maximum DB seq length: 2000000000
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Sequence 191, App
Sequence 41510, A
Sequence 48172, A
Sequence 700, App
Sequence 700, App
Sequence 1292, App
                                Sequence 42, Appl
Sequence 16, Appl
Sequence 47, Appl
Sequence 99, Appl
Sequence 87, Appl
Sequence 587, App
Sequence 587, App
Sequence 41, Appl
                                                                                                                                                                                                                                                                                                   Appl
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Appl
                                                                                                                                                                                    Sequence 50, Appl
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                                                                                                                                                                                                           Sequence 38,
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                                                                                                                                                               US-09-925-301-900
US-09-864-761-43216
US-10-163-866-50
US-09-925-297-747
                                                                                            US-09-739-907-191
US-09-864-761-41510
US-09-864-761-4172
US-10-083-357-700
US-10-083-357-700
US-10-083-357-1292
                        US-10-163-866-41
US-10-163-866-42
US-09-815-923-16
US-09-739-907-99
US-09-739-907-99
US-09-739-907-99
                                                                                                                                                                                                          US-10-163-866-39
US-10-163-866-39
US-10-163-866-43
US-10-163-866-43
US-10-163-866-43
US-10-163-866-43
US-10-163-866-43
US-10-123-866-43
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US-10-137-865-10
US-10-176-918-10
US-10-176-918-10
US-10-140-474-10
US-10-140-474-10
US-10-140-474-10
US-10-140-402-10
US-10-142-43-110
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ALIGNMENTS

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RESULT 1

RESULT 1

US-10-163-866-48

US-10-163-866-48

Sequence 48, Application US/10163866

Publication No US20030027188A1

GENERAL INFORMATION:

APPLICANT: EXELIXIS,

TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

TITLE NET INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USF

CURRENT PILLING DATE: 2002-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR PLICATION NUMBER: US 60/338,733

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-15

PRIOR FILING DATE: 2001-10-15

PRIOR FILING DATE: 2001-0-15

SPIOR PLICATION NUMBER: US 60/357,253

PRIOR FILING DATE: 2002-0-15

NUMBER OF SQ ID NOS: 54

SSCTWARE: PatentIn Version 3.1

SEQ ID NO 48

LENGTH: 501

TYPE: PRI T
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Sequence 2, Application US/08397232A
; Sequence 2, Application US/08397232A
; Patent No. 6180110
; GENERAL INFORMATION:
APPLICANT: EMERSON, SUZANNE U
; APPLICANT: DYCELL, ROBERT H
; FILE REFRENCE: 1925-04-17
; CURRENT FILING DATE: 1939-09-18
; EARLIER APPLICATION NUMBER: 07/947,338
; EARLIER PILING DATE: 1933-09-17
; BARLIER PILING DATE: 1933-09-17
; SEQ ID NO 2
; LENGTH: 227
; TYPE: PRT
; ORGANISM: WILD-TYPE HUMAN HEPATITIS A VIRUS, STRAIN HM-175
US-08-397-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-667-170A-440 (1-2239) x US-08-397-232-2 (1-2227)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                     TYPE: PRT; ORGANISM: Attenuated (4380) HAV, strain HM-175
US-08-475-886-6
                                                                                                                                                            Length:
Matches:
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                                                                                                                                                                                                                                                                                                                       990 AAAGTTGAGGTAAAACCAGCCAGC 967
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8.00
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 2227
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-08-397-232-2
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US-09-667-170A-440 (1-2239) x PCT-US95-04910-14 (1-995)
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Matches:
Conservative:
Mismatches:
Indels:
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FREEDER NO. 6113912
FREEDER NO. 6113912
FREEDER INFORMATION:
APPLICANT: FUNKHOUSER, ANN W
APPLICANT: FURKESON, SUZANNE U
APPLICANT: PURCELL, ROBERT H
APPLICANT: D'HONDT, ERLC
FILE REFERENCE: 20264262023
CURRENT APPLICATION HERATITIS A VIRUS VACCINES
FILE REFERENCE: 20264262023
CURRENT APPLICATION NUMBER: 05/08/475,886A
FARLIER PILING DATE: 1995-09-18
EARLIER PILING DATE: 1995-09-18
EARLIER FILING DATE: 1995-09-18
EARLIER FILING DATE: 1995-03-10
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATCHIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2.
CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 2026-4125PCT
FELECOMMUNICATION INFORMATION:
TELEFAX: (212) 758-4800
TELEFAX: (212) 751-6849
TELEEX: 421792
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 995 amino acids
LENGTH: 995 amino acids
                                                                                                                                                                                                                                                                                  SUFTRACE:

MINISTRACE

APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04910

FILING DATE: 21-APPLICATION

APPLICATION NUMBER: US08/231,526

FILING DATE: 22-APR-1994
                                                                                                                                                                                                          MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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FITLE OF INVENTION: AND VACCINES
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                                                          ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
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8.00
100.00%
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                 NUMBER OF SEQUENCES: 2/
CORRESPONDENCE ADDRESS:
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Best Local Similarity:
Query Match:
                                                                                                                                               USA
                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                 ZIP: 10154
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LENGTH: 2227
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ORGANISM: WILD-TYPE HUMAN HEPATITIS A VIRUS, STRAIN HM-175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Attenuated HAV (Pass 35), strain HM-175
US-08-475-886-4
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Patent No. 6119912
GENERAL INFORMATION
APPLICANT: FUNKHOUSER, ANN W
APPLICANT: EMERSON, SUZANNE U
APPLICANT: EMERSON, SUZANNE U
APPLICANT: D'HONDT, ENLC
TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
FILE REFRENCE: 20264262022
CURRENT APPLICATION NUMBER: 05/08/475,886A
CURRENT FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 07/947,338
EARLIER APPLICATION NUMBER: 08/397,232
EARLIER PILING DATE: 1995-09-18
EARLIER PILING DATE: 1995-09-18
                                                                                                                              Conservative:
Mismatches:
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APPLICANT: EMERSON, SUZANNE U
APPLICANT: EMERSON, SUZANNE U
APPLICANT: PURCELL, ROBERT H
APPLICANT: D'HONDT, ERIC
TITLE OF INVENTION: HEPATITIS A VIRUS VACCINES
FILE REFRENCE: 20264262US2
CURRENT APPLICATION NUMBER: US/08/475,886A
CURRENT FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-09-18
EARLIER FILING DATE: 1995-09-18
EARLIER FILING DATE: 1995-09-18
EARLIER FILING DATE: 1995-03-10
NUMBER OF SEQ ID NOS: 6
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Matches:
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; Sequence 4, Application US/08475886A
; Patent No. 6113912
; GENERAL INFORMATION:
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                                                                                                                       Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
                                                                Alignment Scores:
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LENGTH: 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                  US-08-475-886-2
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                                                                                                                                                                       Query Match:
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APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-667-170A-440 (1-2239) x US-09-012-710-10 (1-793)
                                                                                            US-09-667-170A-440 (1-2239) x US-09-556-273-11 (1-786)
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Mismatches:
Indels:
Conservative:
                   Mismatches:
Indels:
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411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600-1-194
                                                                                                                                                                                                                           US-09-012-710-10; Sequence 10, Application US/09012710; Patent No. 6087478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 AsnSerMetSerValSerTrpSer 556
                                                                                                                                                      549 AsnSerMetSerValSerTrpSer 556
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                                                                                                                                  766 AATAGCATGAGTGTCAGCTGGAGC 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                     Query Match:
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US-09-556-273-10

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APPLICANT: The Government of the United
APPLICANT: States of America as represented
APPLICANT: States of America as represented
APPLICANT: By the Secretary, Department of
APPLICANT: Health and Human Services
TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL PRIMATE T-CELL
TITLE OF INVENTION: LYMPHOTOPIC VIRUS AND THE USE OF THIS VIRUS
TITLE OF INVENTION: DECOMPONENTS THEREOF IN DIAGNOSTIC ASSAYS
                                                              APPLICANT: Vinkemeier, Uwe
APPLICANT: Vinkemeier, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Moarefi, Jr., James E.
APPLICANT: Willyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-667-170A-440 (1-2239) x US-09-556-273-10 (1-793)
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Mismatches:
                                                                                                                                                                                                                                                     ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 14, Application PC/TUS9504910 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/556,273
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 10, Application US/09556273 Patent No. 6312887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/012,710
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INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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100.00%
1.09%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                          New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                          Patent No. 6312887
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                     07601
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GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Ruriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
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Mismatches:
Indels:
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STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                   NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0514 US
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-855-0555
TELEFRAX: 650-845-4166.
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OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 515 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
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100.00%
100.00%
1.09%
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                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                       GenBank
                                                                                                                                                                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                         MEDLAL
LIBRARY: Geneu...
LIBRARY: 1665759
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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APPLICANT: Vinkemeier, Uwe
APPLICANT: Vinkemeier, Uwe
APPLICANT: Woarefi, Ismail
APPLICANT: Moarefi, Jr., James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
                                                                                                                                                                                                                                                                     US-09-667-170A-440 (1-2239) x US-09-012-710-11 (1-786)
                                                                                                                                                                             Conservative:
                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
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Matches:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
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INFORMATION FOR SEQ ID NO: 11:
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LENGTH: 786 amino acids
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NO
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USA
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TYPE: amino acid
                                 linear
                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                STRANDEDNESS:
                               TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL: N
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Sequence 3, Application US/09243920
Patent No. 5981242
GENERAL INFORMATION
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TILLO F INVENTION: AMINO ACID PERMEASE HOMOLOG
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-667-170A-440 (1-2239) x US-09-073-362-3 (1-515)
                              SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00 // FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/243,920
FILING DATE:
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Matches:
                                                                                                                                                                                           APPLICALE
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CERTON, Michael C
REGISSTRATION NUMBER: 39,132
REGISSTRATION NUMBER: PF-0514 US
TELECOMMUNICATION INFORMATION:
"PRIEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/073,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          517 TATGCTGAATTGGGAACAACTATA 540
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                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3:
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MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
1.09%
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acids
TYPE: amino acid
STRANDEDNESS: single
       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 31/4 ...
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OPERATING SYSTEM:
SOFTWARE: FASTSEC
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Best Local Similarity:
Query Match:
                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-243-920-3
                                                  GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09073362
Patent No. 5942399
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Cocley, Neil C.
TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STRRET: 3174 Porter Drive
                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-667-170A-440 (1-2239) x US-09-071-035-306 (1-275)
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Mismatches:
Indels:
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Matches:
                                                                                                                                                  ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMNUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 306:
SEQUENCE CHARACTERISTICS:
                   ; Sequence 306, Application US/09071035; Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437 AGCACGCCTTAGGAGATGAAG 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 amino acids
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PRIOR APPLICATION DATA:
                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-09-071-035-306
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                        ZIP: 20850
                                                                                                                                                 ADDRESSEE:
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US-09-071-035-306
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GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                          US-09-667-170A-440 (1-2239) x US-09-073-362-1 (1-511)
                                                                                                                                                                                                                                                                                                                                                                              517 TATGCTGAATTGGGAACAACTATAAAGAAATCTGGA 552
                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39,132
FR: PF-0514 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/073,362
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09243920 Patent No. 5981242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
             SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: ESOGITUO2
CLONE: 2667831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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100.00%
100.00%
1.64%
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LENGTH: 511 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: Single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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Best Local Similarity:
Query Match:
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; CLONE: 2667831
US-09-243-920-1
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                                                                                                                                                            US-09-073-362-1
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Sequence 308, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INFORTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-667-170A-440 (1-2239) x US-09-071-035-308 (1-241)
                                                                                                                                              US-09-667-170A-440 (1-2239) x US-09-243-920-1 (1-511)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
                                                  Conservative:
Mismatches:
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                                    Matches:
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                                                                                         Indels:
                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 AGCACGCCTTAGGAGATGAAG 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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8.00
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                    Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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                       Pred. No.:
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                                          Score:
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RESULT 4

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FILING DATE: CLASSIFICATION:
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STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-073-362-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
Command line parameters:
-MODEL-frame+_n2p.model -DEV=x1h
-0=0x002_121223/app_query.fasta_1.2375
-0=0x02_1/USPT0_spool/US09667170/runat_04042003_091002_21223/app_query.fasta_1.2375
-DB=ISsued_Patents_AA -OFWT=fastan -SUFFIX=olin2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=0ligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFNT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09667170_eCGN_1_1_17_eunat_04042003_091002_21223 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NGS_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 308, App
Sequence 306, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 11, Appli
                                                                                                      (without alignments)
7121.938 Million cell updates/sec
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                                                                                                                                                                         Description
                                                                                    April 16, 2003, 16:33:19; Search time 18.5 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/FB_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/FB_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

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US-09-243-920-1

US-09-071-035-308

US-09-071-035-308

US-09-073-35-33

US-09-012-710-11

US-09-556-273-11

US-09-556-273-10
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                   ), Xgapext 60.0
), Ygapext 60.0
), Fgapext 7.0
                                                                                                                                                                                                                                                              7.0
                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                , Fgapext
, Delext
                                                                                                                                              US-09-667-170A-440
                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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Ygapop 60.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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                                                                                                                                           Title:
Perfect score:
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                                                         OM nucleic
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                                                                                    Run on:
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Appl Appl Appl

Sequence 11,

Seguence 14, Seguence 2,

PCT-US95-04910-14 US-08-475-886-2

Sequence 1 Sequence 1 Sequence 1

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44, Appl
44, Appl
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TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                  US-08-406-330-44
US-08-56-597-44
US-08-642-255-8
US-08-817-548A-3
US-08-940-095-156
US-08-940-095-156
US-08-940-095-172
US-08-940-095-172
US-08-940-095-172
US-08-940-095-175
US-08-940-093-156
US-08-940-093-156
US-08-940-093-156
US-08-940-093-166
US-08-940-093-184
US-08-940-093-184
US-08-940-093-184
US-08-940-093-184
US-08-940-093-184
US-08-940-093-184
US-08-940-093-184
US-08-940-093-184
US-08-940-093-184
                                                                 US-08-397-232-4
US-09-171-387-2
US-09-653-499-2
US-09-653-499-4
US-09-653-499-6
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US-09-465-719-156
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APPLICATION NUMBER: US/09/073,362
-08-475-886-6
-08-397-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0514 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/09/073,362
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Patent No. 5942399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillman, Jennifer L.
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Hillman,J.L., Yue,H. and Corley,N.C.
Anino acid permease homolog
Patent: US 5981242-A 2 09-NOV-1999;
                                             Sequence 2 from patent US 5981242.
AR084930
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1020 AACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGAC 1079
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                                                                                                           972 CAATGIGGCCTATIATACIGIGCIAGACATGAGAGACATCTIGGCCAGTGAIGCTGITGC 1031
                   912 GAACCTGCCCTCTCCATTGCCATCTCCATGCCCATTGTCACCATCTATATCTTGAC
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FFVGSREGHLPDAICMIHVERFTPVPSLLFNGIMALIYLCVEDIFQLINYSFSYWFF
VGLSIVGQLYLRWKEPDRPRFKLSVPFPIVFCLCTIFLVAVPLYSDTINSLIGIAIA
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LIVGNMIGSGIFVSPKGVLIYSASFGLSLVIWAVGGLFSVFGALCYAELGTTIKKSGA
SYAYILEAFGGFLAFIRLWTSLLIIEPTSQAIIAITFANYMVQPLFPSCFAPYAASRL
                                                                             PRI 15-AUG-2000
                                                                                                                                                                                                                                                                                                                      Submitted (23-FEB-1998) Kiyoshi Takayama, Taisho Pharmaceutical Co, Ltd., Molecular Biology Laboratory; Yoshino-cho 1-403, Ohmiya, Saitama 330, Japan (E-mail:s16777@ccm.taisho.co.jp, Tel:+81-48-663-1111, Fax:+81-48-652-7254)
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/note="similar to a amino acid permease"
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/db_xref="G1:9836572"
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/db_xref="taxon:9606"
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Takayama, K. and Yoshimoto, M.
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291 TAAGAAATCTGGGGCCAGCTATGCCTATATCCTGGAGGCCTTTGGAGGATTCCTTGCTTT 350
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GEGGGYEDLEKBERSTEGTSTNVGQWYLALYSCILFATGGWYLIFVVERBHIEPYKNLDR
ALIISMAIVTLYVYLTINLAYFTTLFPEQMLASEAVANDFGNYHLGVVAAMIIEVVVGLS
CFGSVNGSLFTSSRLFFVGAREGHLPSLLAMIHPRLITPMPSLLIFTCAMTLLYAFSDD
FYRYINFSFRWLCYALAIIGMMWIAYKKPELERPIKVNILLPIFFTLACIFLIVVS
FYRYINFSCGIFIILLGGWWYFFGVWWQNKPDMILHGIHSSTALLGKVWEAVPQES"
501 C 361 C 361 G 361 C
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ELQRTITLVNGVAIIVGTIIGSGIFVTPTGVLREAGSPGLSLLVWAVCGLFSIVGALC
YAELGTTISKSGGDYAYVLEVYGALPAFLKLWVELLIIRPSSQYIVALVFATYLLKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-AUG-1997) Lab. of Mol. Embryology, National Institute of Child, Health and Human Development, NIH, Building 18T, Rm 106,
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                                   VRT 16-MAR-1999
                                                                                                                                                                                                              (bases 1 to 2263)
Torents.D., Estevez.R., Pineda,M., Fernandez,E., Lloberas,J.,
Shi,Y.B., Zorzano,A. and Palacin,M.
Identification and characterization of a membrane protein (y+L
amino acid transporter-1) that associates with 4F2hc to encode the
amino acid transport activity y+L. A candidate gene for lysinuric
                                     Xenopus laevis L amino acid transporter-1 LAT-1 mRNA, complete cds. AF019906
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 GTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGCACCATC 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="L amino acid transporter-1 LAT-1"
/protein_id="AAB93541.1"
/db_xref="GI:2731774"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 585; Indels
                                                                                                                                                                                                                                                                                                                      protein intolerance
J. Biol. Chem. 273 (49), 32437-32445 (1998)
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ilarity 55.4%; Pred. No. 6.7e-76;
Conservative 0; Mismatches 5R5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="transmembrane protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Xenopus laevis"
                                 2263 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bethesda, MD 20892, USA
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                                                                                                                                                                                               Xenopodinae; Xenopus.
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Shi,Y.
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639
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                                                                                                                                                                                                                                                                                                                                                           TGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGGCATAACTGTAGTGATG
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580 TTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCA
                                                                                                                                                                           640 GCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTCTGGAACCATTTTTATTCAA
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                                                                                   646 TACGGTGCGCTGCCGCCTTCCTAAAGCTCTGGGTGGAGCTGCTCATCATCCGGCCCTCG
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Ohara.O., Nagase.T., Kikuno,R. and Nomura,N.

Direct Submission

Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)

Location/Qualifiers
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TTITKSGASYAYILEAFGGFIAFIRLWVSLLVVEPTGQAIIAITFANYIIQPSFPSCD
PPYLACRLLAAACICLLTFVNCAYVKWGTRVQDTFTYAKVVALIAIIVMGLVKLCQGH
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IVTLIYILTNVAYYTVLNISDVLSSDAVAVTFADQTFGMFSWTIPIAVALSCFGGLNA
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SLIGIGIALSGVPFYFMGVYLPESRRPLFIRNVLAAITRGTQQLCFCVLTELDVAEEK
Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of CNRA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489
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                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 273 (49), 32437-32445 (1998) 99047611
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/db_xref="G1:1665759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HA7016"
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/cell_type="Myeloblast"
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262. .1809
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                                                                                                                                                                                                                                        TITGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC
                                                                                                                                                                               730 CCCAGCTGTGATCCCCCATACCTGGCCTGCCGTCTCCTGGCTGCTGCTTGCATATGTCTG
                                                                                                                                                                                                                                                                                       814 TITIGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAA
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                                   610 GAGGCCTTTGGGGGCTTCATTGCCTTCATCCGCCTGTGGGTCTCACTGCTAGTTGTTGAG
                                                                       CCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGTACATTCTGGAACCATTTTTT
                                                                                                                                                                                                                   GTGATGGTCCTAAATAGCATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACC
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/translation="MEAREPGRPTPTYHLVPNTSQSQVEEDVSSPPQRSSETMQLKKE
ISLLNGVSLVVGNMIGSGIFVSPKGVLVHTASYGMSLIVWAIGGLFSVVGALCYAELG
TTITKSGASYAYILEAFGGFIAFIRLMVSLLVVEPTGQAIIAITFANYIIQPSFPSCD
Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J.,
Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                             information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPYLACRLLAAACICLLTFVNCAYVKWGTRVQDTFTYAKVVALIAIIVMGLVKLCQGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVTLIYILTNVAYYTVLNISDVLSSDAVAVTFADQTFGMFSWTIPIAVALSCFGGLNA
SIFASSRLFFVGSREGHLPDLLSMIHIERFTPIPALLFNCTMALIYLIVEDVFQLINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSFSYWFFVGLSVVGQLYLRWKEPKRPRPLKLSVFFPIVFCICSVFLVIVPLFTDTIN
SLIGIGIALSGVPFYFMGVYLPESRRPLFIRNVLAAITRGTQQLCFCVLTELDVAEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEHFQDAFEGSSWDMGNLSLALYSALFSYSGWDTLNFVTEEIKNPERNLPLAIGISMP
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                                                                                                                     Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 62 Row: h Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 ACCATCATTGGAGCAGGAATCTTCATCTCCTAAGGGCGTGCTCCAGAACACGGGCAGC 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="solute carrier family 7 (cationic amino transporter, y+ system), member 6" /protein_id="AAH28216.1" (db_xref="GI:20381372")
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                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon.9606"
/clone="MGC:40002 IMAGE:5214340"
/tissue_type="Blood, adult leukocytes"
/clone_lib="NIH_MGC_118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.9%; Score 379.2; DB 9 55.9%; Pred. No. 8.7e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="LocusID:9057"
                                                                                                                                                                                                                                              Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                951 ACAGAAGAAATCAAAAACCCAGAAAGAAATTTGCCCTTGGCCATTGGGATTTCTATGCCA 1010
                                                                                                                                                                                                                                                                                                                                                                                               1011 ATTGTGACGCTCATCTACATCCTGACCAATGTGGCCTATTACACAGTGCTGAACATTTCA 1070
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CTGACATTTGTGAACTGTGCCTATGTCAAGTGGGGCACACGTGTGCAGGACACGTTCACT 770
                                       873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens male bone marrow Myeloblast cell_line:KG-1 cDNA mRNA, clone_lib:pBluescript II SK clone:HA7016.
                                     814 TITIGCAAGCICACAGCAATICIGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAA
                                                                                                                   GGTCAAACGCAGAACTTTAAAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG
                                                                                                                                          1054 ATTGTCACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTG
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                                                                                                                                                                                               1114 GAGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTC
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D87432
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KIAA0245.
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/note="similar to Bos taurus EST AW669076 (NID:97525590)"
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/rpt_family="Alu"

6899. .7362

/note="match to EST AA488687 (NID:g2216118) ab38f03.sl"

6970. .7746
                                                         /note="match to EST B1497113 (NID:915336457)"
4359. 4476
/note="match to EST AA227760 (NID:91849333) zr56a07.rl"
4404. 5178
              to EST A1267688 (NID:93886855) aq93c10.x1"
                                                                                                                                                                                                                                                                                                                                                                                              /note="match to EST N80420 (NID:g1243121) y292e06.rl" 5255. .6002
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6140. .6518
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/note="similar to EST BM547723 (NID:918781736)"
4859. .5265
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/note="match to EST BG254117 (NID:g12763933)"

/note="match to EST BF084219 (NID:g10878049)"

5074. .5447
                                                                                                                                                                                                                                                                                                                                                                                                           'note="match to EST BE739933 (NID:g10153837)"
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7124. 7125
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7253. 7884
                                                                                                                            /note="match to EST BG291471 (NID:g13049386)"
4412. .4619
                                                                                                                                                                                                                                                                                 4859. .5265--- ... ... ... ... ... ... (NID:918781734
/note="match to EST AW901105 (NID:98065310)"
5002. .5687
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//note="match to EST AA471165 (NID:92199022)"
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/note="match to EST AW996897 (NID:g8257131)"
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7174. 7495
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/note="match to EST AA307001 (NID:91959330)"
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5442. .6151

547. .5830 (NID:98150887)"
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6032. .6836
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5782. .6124
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5875. .6701
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/note="similar to Homo sapiens EST BG499179
(NID:913460696)"
                                                                                                                            4412. 4619 ... ... bG291471 (NID:g13049386 /note="similar to Homo sapiens EST BF154977 (NID:g11050160)"
                                .153. .4433
'note="match to EST C00538 (NID:91432768)"
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Pred. No. 2.9e-114;
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8035. .8572
1137. .4527
/note="match
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3448 bp mRNA linear PRI 01-MAY-2002 Homo sapiens, solute carrier family 7 (cationic amino acid transporter, y+ system), member 6, clone MGC:40002 IMAGE:5214340, BC028216
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,Q.L.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11335 TATATGGGTTTTGTAAAGATGGTTTTACACACTATAGATGTCTATACTGTGAAAAGTGTT 11276
TATATGGGTTTTGTAAAGATGGTTTTACACACTACAGATGTCTATACTGTGAAAAGTGTT 2150
                                                                                                                                                                                     1791 TTACTTCATTTTCTGAAGICTAGAGAATTACAACTTTGGTGATAAACAAAAGGGGTCA 1850
                                                                                                                                                                                                                                                                                 GTTATTTTTATTCATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAA 1910
                                                                                                                                                                                                                                                                                                                                                                          CTCTATGTAGTATAGAAAGTGAATATGCAGTTATTCTATGAGTCGCACAATTCTTGAGT 1970
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Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Prerayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1971 CTCTGATACCTACCTATTGGGGTTAGGAGAAAAGACTAGACAATTACTATGTGGTCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTACAACATATGTTAGCACGCAAAGAACCTTCAAATTGAAGACTGAGATTTTTCTGTA
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ACLIU804 64196 bp DNA linear PRI 30-MAR-2002 Homo sapiens BAC clone RP11-725C19 from 4, complete sequence. AC110804
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4 (bases 1 to 64196)
Waterston, R.H.
Direct Submission
Submitted (06-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (21-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missouri 63108, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1974 TGATACCTACTATTGGGGTTAGGAGAAAGACTAGACAATTACTAT-----GTGGTC 2026
                                          2057 GTGCCTATCTGCTGGGGGAAAGGAAAAAACCTAAGGGCTTTGGTACCTGGGCTATCA 2116
                                                                                                             Direct Submission
Submitted (15-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                     2027 ATTCTCTACAACATATGTTAGCACGCCAAAGAACCTTCAAATTGAAGACTGAGATTTTTC
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Submitted (30-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Mar 21, 2002 this sequence version replaced gi:19073866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 64196)
Pearman, C., Kozlowicz, A. and Dignan, G.
The sequence of Homo sapiens BAC clone RP11-725C19
Unpublished (2001)
                                                                                                                                                                                                2177 TGTATATATGAGGTCTATAAACATAGCTTTACCTACT 2213
                                                                                                                                                                          2087 TGTATATAGGTTTTGTAAAGATGGTTTTACACACT 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 64196)
Sulston, J.E. and Waterston, R.
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Center: Washington University Genome Sequencing Center

Web site: http://genome.wustl.edu/gsc

code: WUGSC

Contact: sapiens@watson.wustl.edu Center project name: H_NH0725C19 Summary Statistics

This sequence was finished as follows unless otherwise noted:

chemistry, or covered by high quality data (i.e., phred quality >= 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by all regions were double stranded, sequenced with an alternate restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McDherson, Department of Genetics, Washington University, St. Louis MG. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J. J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: DRACA23 & The RPCI-11 human BAC library was made from the blood of one VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RPI1-8P17, 2000 bp overlap. Actual start of this clone is at base position 185268 of RPI1-393A12; actual end is at base position 64196 of RPI1-725C19.

Polymorphisms exist between AC013365 and AC110804. Location/Qualifiers 1. .64196

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source
FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.0%; Score 1208.6; DB 10
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Conservative 0; Mismatches 324;
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| 526 c 509 g 639
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Matches 1548; Conserv
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                                                                                                                             CAGGACTGATTTATCTTCGATACAAACGCCCAGATATGCATCGTCCTTTCAAGGTGCCTC
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                                                           Score 1373.4; DB 9; Length 2000;
Pred. No. 1.4e-313;
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Mus musculus xCT mRNA for cystine/glutamate transporter, complete
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Cloning and expression of a plasma membrane cystine/glutamate exchange transporter composed of two distinct proteins
J. Biol. Chem. 274 (17), 11455-11458 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission.
Submitted (13-JAN-1999) Hideyo Sato, University of Tsukuba,
Institute of Basic Medical Sciences; Tennodai 1-1-1, Tsukuba,
Ibaraki 305-8575, Japan (E-mail:hideyo-s@md.tsukuba.ac.jp,
Tel:81-298-53-3282, Fax:81-298-53-3039)
                                                                                                     1109 TCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGCTGTCTCCAGGTTATTCTATGTTG
1142 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCC
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Sato, H. and Bannai, S.
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                                       GCTGGACCCCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGAATTCTGATAA
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                                                                                                  CATTTGGACGCTACATTCTGGAACCATTTTTTATTCAATGTGAAATCCCTGAACTTGCGA
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                                                                                                                                           TACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGG
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                             482 TGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAA
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/translation-"MYRRPVYSTISKGGYLQGNVNGRLPSLGNKEPFGQEKVQLKRKV
TLLRGVSTIIGTIGGAGIFISPKGVLQNGSVGWSLTIWPVGCVLSLFGALSYRAELGT
TIKKSGGHYTYILEVFGPLPARVRWVELLIIRPARATVISLARGRYILEPFFQCEI
PELAIKLITAVGITVVMVLNSMSVSWSARIQIFLTFCKLTAILIIIVPGVMQLIKGGT
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VTIGYVLTNVAYFTTINAEELLLSNAVAVTFSERLLGNFSLAVPIFVALSCFGSMNGG
VFAVSRLFYVASREGHLPEILSMIHVRKHTPLPAVIVLHPLTMIMLFSGDLDSLLNFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim,J.T., Chairoungdua,A., Cha,S.H., Segawa,H., Matsuo,H., Kim,D.K., Endou,H. and Kanai,Y. Human cystine/glutamate exchanger: cDNA cloning and upregulation by oxidative stress in glioma cells.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens hxCT mRNA for cystine/glutamate exchanger, complete
                                                                                                                                                                                                                                                                Submitted (01-APR-2000) Yoshikatsu Kanai, Kyorin University Sc of Medicine, Department of Pharmacolgy and Toxicology; 6-20-2 Shinfaka, Tokyo 181-8611, Japan (E-mail: Xanai@kyorin-u.ac.jp, Tel:+81-422-47-5511(ex.3453), Fax:+81-422-79-1321)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens adult cDNA to mRNA, clone_lib:brain cDNA library
                   CGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATT
                                                                               ATCTCTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAA
                                                                                                                                                               1682 CCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAAGATAAGTTATGAACTAATG
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/protein_id="BAB40574.1"
/db_xref="GI:13316846"
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/db_xref="taxon:9606"
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1819 ITCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAA 1860

qq	739	TCAAGCTCATTACAGCTGTGGGCATAACTGTGATGGTCCTAAATACCATGAGTGTCA 798	
Qy	782	GCTGGAGCGCCCGGATCCAGATTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATAA 841 	
oy D	842	TTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCCT 901 	
Qy Db	902	ATGTATG 96	
oy Ob	962	CATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCTGAAAAAA 1021 	
Qy	1022	CCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGTGGCGACAA 1081 	
Oy Dp	1082	ATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAG 1141 	
oy Db	1142	TGACCTTTTCTGAGGGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCC 1201 	
Qy Db	1202	TCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTG 1261 	
Qy Db	1262 1279	CGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTC 1321 	
Qy Db	1322	CTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGACC 1381 	
Qy Db	1382	TCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTTATTGGCCTGGCAGTTG 1441 	
Oy do	1442	CTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCAC 1501 	
oy Op	1502	TGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTATT 1561 	
Qy Dp	1562	CGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATT 1621 	
Qy	1622	80 00	
Oy Dp	1682	CCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAAGATAAGTTATGAACTAATG 1741 	
QY	1742	GACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAAATAGGGATTTTTACTTCATT 1801 	
δy	802	GAAAGCTAGAGAATTACAACTTTGGTGATAAAGAAA 1843	

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VTIGYVLTNVAYFTTINAELLISNAYAYFSBRLGARSLAAPPIFYALSCFGSWNG
VFANSRLFYVSREGLIFEISMINYRHTPLPAVIVLHPLTMIMLFSGDLDSLLNFI
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GIGFVITLTGVPAYYLFIIWDKKPRWFRIMSEKITRTLQIILESVPEEBDKL"
                                                   PRI 10-FEB-2001
                                                            Homo sapiens mRNA for cystine/glutamate transporter, complete cds. AB026891
                                                                                                                                                                                                                                                          1 (sites)
Sato,H., Tamba,M., Kuriyama-Matsumura,K., Okuno,S. and Bannai,S.
Molecular cloning and expression of human xCT, the light chain of amino acid transport system xc-
Antioxidants and Redox Signaling 2, 665-671 (2000)
2 (bases 1 to 1861)
Sato,H. and Bannai,S.
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (30-APR-1999) Hideyo Sato, University of Tsukuba,
Institute of Basic Medical Sciences; Tennodai 1-1-1, Tsukuba,
Ibaraki 305-8575, Japan (F-mail:hideyo-s@md.tsukuba.ac.jp,
Tel:81-298-53-3282, Fax:81-298-53-3039)
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                                                   linear
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/protein_id="BAA82628.1"
/db_xref="GI:5668545"
                                                   mRNA
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Homo sapiens fibroblast cDNA to mRNA.
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/db_xref="taxon:9606"
/cell_type="fibroblast"
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236. .1741
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TLLRGYSI LIGHT IGAE IF SEPKGYLQCNVGSGMSLTIMTVGCYLSLEGGALSYABLGT
TLLRGYSI LIGHT IGAE IF SEPKGYLQUTGSYGMSLTIMTVGCYLSLEGGALSYABLGT
TEKRSGGHYTY ILEVFGPLAFVYNWVLELI IRPAATAVI SLAFGRY ILEPFFIQCEI
PELAIKLITAYGITTVWHYLNSMSYSWSARIQI PELTFCKLTAILI ILTVPGVWQLLKGOT
ONFKDAFSGRDSSITRLPLAFYXGWYAYAGWFYLNFYTEVNPEKTINDAICI SMAI
VTGSYLTNYNAY FITINAGELLLSNANAVI PESERLLGNFSLANDI FYALSCFGSMNGG
VFRAGSRLFYVASREGHLPELLSMIHYRKHTPLPAYI VLHPLTMIMLSGGLLSLNFI
SFARMLFIGLAVAGLIYLRYKCPDMHRPFKVPLFIPALFSFTCLFWYALSLIYSDPFST
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                                                                                                                                                                                                                                                                             /product="calcium channel blocker resistance protein
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CD98 light chain implicated in redox control and
                                                                                                    Spring Harbor Labs, 1 Bungtown
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                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="fibrosarcoma HT1080"
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0; Mismatches
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Conklin,D.S. and Beach,D.H.
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Homo sapiens calcium channel blocker resistance protein CCBR1 mRNA,
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Db 1854		qq	299 GGCTGCCTTCCCTGGGCA
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		Oy Oy	365 CTTTACTGAGGGGAGTCT
Db 2034		qu	425 CTCCTAAGGGCGTGCTCC
Qy 2162 Db 2094	2 AAAAAAGCATACATCATGATTATGGCAAAGAGAGAA 2200 	do oy	482 TGTGTGGGGTCCTGTCAC
RESULT 5 AF252872		da da	542 AGAAATCTGGAGGTCATT
DEFINITION ACCESSION VERSION	Ar5J20/2 Ar62 DP MKNA 11near PKI U2-MAY-2001 NH Homo sapiens cystine/glutamate transporter xCT mKNA, complete cds. Ar5J2872 AP552873 GT-13924719	ov q	602 TACGAGTCTGGGTGGAAC
KEYWORDS	Homo sapiens.	ra ko	
ORGANISM	M HOMO Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Enthoria: Drimatos: Catarchis: Homisaiass: Futeleostomi;	qu	665 CATTTGGACGCTACATTC
REFERENCE AUTHORS	Talmariar, Editoriar Filmares, Carallilli, HOMILLIAGE; HOMO. Chancy,C.D., Kekuda,R., Wang,H., Huang,W., Prasad,P.D., Smith,S.B.	QY	722 TCAAGCTCATTACAGCTG
TITLE	and Ganapathy,V. Structure, Function and Regulation of Human Cystine/Glutamate	qa	725 TCAAGCTCATTACAGCTG
JOURNAL	Transporter in Retinal Pigment Epithelial Cells Unpublished 1 (heart 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ογ	782 GCTGGAGCGCCCGGATCC
AUTHORS	 Z (Joses 1 to 2402) Wang A. P. Sad, P. D. and Ganapathy, V. 	ପୁପ	
JOURNAL	AL Submitted (05-APE-2000) Biochemistry & Molecular Biology, Medical College of Georgia, 1120 15th Street, Augusta, GA 30912, USA	δλ O	842 TTATAGTCCCTGGAGTTA
FEATURES Sourc	Location/Qualifiers	^0	
	/organism="Homo sapiens" /db_xref="taxon:9606"	qa T*	
CDS	/tissue_type="placenta" 223. 1737	QY	
	/Codon_start=1 /product==rystine/glutamate transporter xCT" /protein id=labk401111"	QQ	965 CATAIGCIGGCIGGIITI
	/f_xrcan_====================================	Qy	1022 CCATTCCCCTTGCAATA
	TLERGVSTICST TILKGVSTICSTICSTEPSKGVLOVGSVGMSTIVTVCGVLSLFGRSYAGGT TIKKSGGHYTY LIEVFGPLPARYWWELLI TRPAATAVISLAGGTF	qa	1025 CCATTCCCCTTGCAATAT
	PELAIKLITAVGITVVMYLNSMSYSWSRRIQIFELTFCKLTAILIIINTEGOT QNFKDAFSGRDSSITRLPLAFYYGMYAYAGWFYLNFVTEEVENPEKTIPLAICISMAI	QY	1082 ATGTGGCCTACTTTACGA
	VTIGYVLTNVAYFTTINAEELLLSNAVAYFSERLGNFSLAVPIFVALSCFGSMNGG VFAVSRLFYVASREGHLPEILSMIHVRKHTPLAAVIVLHPLTMIMIFSGNINSFINFL	Dβ	1085 ATGTGGCCTACTTTACGA
BASE COUNT	SFARWLFIGLAVAGLIYLRYKCPDMHRPFKVPLFIPALFSFTCLFMVALSLYSDPFST GIGFVITLTGVPAYYLFIIMDKKPRWFRIMSEKITRTLQIILEVVPEEDKL" T 735 a 484 c 521 q 742 t	QY	1142 TGACCTTTTCTGAGCGGC
ORIGIN		3	
Query Match Best Local Si Matches 1965:	84.38; Score 1888.2; DB 9; Length 2482; milarity 97.18; Pred. No. 0; Conservative 0. Mismatches 3: Indole 55.	Oy Dp	1202 TCTCCTGCTTTGGCTCCA
Qy 182	CCTGTTGTGCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGG 241	Qy Ph	1262 CGTCTCGAGAGGGTCACC
	GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGA 298	à V	
Oy 242	242 GGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACG 301	· _	

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                                                                SECCTTTTCAGGAAGAGAAAGTGCAGCTGAAGAGGAAAGTCA
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/lab_host="DH10B-R"
                                                                                                                                                                                                                                                         Length 2155;
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       /db_xref="taxon:9606"
/clone="MGC:20026 IMAGE:4562994"
                                                                                                                                                                                                                                                         Score 1888.2;
Pred. No. 0;
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                                                      /note="Vector: pOTB7"
161. .1666
                                                                                 /codon_start=1
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96.9%;
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                                                                                            CATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAAAACCCTGAAAAAA 1021
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                                                                                                                                                                                            ATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAG
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TCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGT 	 CUIGGAGCGCCGGATCCAGAITITCTIAACCTITIGCAAGCTCACAGCAAITCTGATAA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	2 TFATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCT 	2 TTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTATG 	2 CATATGCTGGCTGGTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAAA	2 CCATTCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAA	PAGEGCCTACTTTACGACCATTAATGCTGAGGACCTGCTGCTTTCAAATGCAGTGGCAG	FGACCTTTCTGAGGGGCTACTGGGAAATTTCTCATTAGCAGTTCGGATCTTGTTGCTGCCCCCCCC	TCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGCTGTCTCC	CGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTC	CTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTCTGGAGAGC	TCGACAGTCTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTATATTGGGCTGGCAGTTG 	CTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTIIIIIIIIII	TGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTATT	CGGACCCATTAGTACAGGGATTGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTATT	ATCTCTTTATATATAGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAA	CCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAAGATAAGTTATGAACTAATG 	GACTTGAGATCTTGGCAATCTGCCCAAGGGAGACACAAAATAGGGATTTTACTTCATT 	TTCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAAGGAGTCAGTTATTTTAT
20 00 0	554	842	902	962	1022 794	1082	1142	1202 974	1262	1322	1382	1442	1502	1562	1622 1394	1682 1454	1742	1802
6 G 6	g G	Qy Dp	Qy Dp	Oy Dp	Oy Dp	Qy Db	Oy Dp	Oy Dp	Qy Dp	Qy Dp	Qy	Qy Db	Qy	Qy	Qy Db	Qy Db	Oy Db	Οy

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PRI 06-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens, Similar to solute carrier family 7, (cationic amino acid transporter, y+ system) member 11, clone MGC:20026 BC012087
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
1922 TATAGAAAGTGAATATGCAGTTATTCTATGAGTCGCACAATTCTTGAGTCTCTGATACCT 1981
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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BC012087.1 GI:15082351
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo saplens mRNA for cystine/glutamate transporter (XCT gene).
AJ277882
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GIGFVITLTGVPAYYLFIIWDKKPRWFRIMSEKITRTLQIILEVVPEEDKL"
                                                                                                                                                                                                                                                                                                                         /translation="MYRRPVYSTISKGGYLOGNYNGRLPSLGNKEPPGGEKVQLKRKY
TLLRGVSIIIGTIIGAGIFISPKGVLQNTGSYGMSLTIWTVCGVLSLFGALSYAELGT
TIKKSGGHYTYILEVFGPLPAFVRVWVELLIIRPAATAVISLAFGRYILEPFFIQCEI
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and Medicine, Via Olgettina 58, 20132 Milan, ITALY
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/protein_id="CAC81905.1"
/db_xref="G1:18073362"
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                                                    /organism="Homo sapie
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                                                                                              /chromosome="4"
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Matches 1966; Conservative
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/gene="XCT"
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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April 16, 2003, 03:54:58 ; Search time 6493 Seconds (without alignments) 10035.605 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-667-170A-440

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Perfect score: Sequence: Scoring table:

2054640 seqs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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ALIGNMENTS

PAT 15-DEC-2001	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Reed,S.G., Lodes,W.J., Mohamath,R., Secrist,H., Benson,D.R., Indirias,C.Y., Henderson,R.A., Fling,S.P., Algate,P.A., Elliot,M., Mannion,J. and Kalos,M.D.
linear	Vertebrata i, Hominida	rist,H., Ber P., Algate,1
p DNA 2295.	Craniata; Catarrhin	h, R., Sec Fling, S.
AX321909 2239 bp Sequence 440 from Patent W00172295 AX321909 1 GT-17906515	n. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	*Red,S.G., Lodes,W.J., Mohamath,R., Secrist,H., Benson,D.R., Indirias,C.Y., Henderson,R.A., Fling,S.P., Algate,P.A., Elli Mannion,J. and Kalos,M.D.
AX321909 Sequence 440 from Paten AX321909 AX321909 1 GT-17906515	human. Homo sapiens Eukaryota; Metaz Mammalia; Euther	Reed,S.G., Lodes,M.J., Mo Indirias,C.Y., Henderson, Mannion,J. and Kalos,M.D.
		Reed, S Indir:
RESULT 1 AX321909 LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM REFERENCE	AUTHORS

9. Pp 9.	340	GTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGCACCATC 399 11	
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οy	700	TGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGGATAACTGTAGTGATG 759	
QQ	556	TGTCCCGTGCCCGAGGAGGCTGCCAAGCTCGTGCTCTCTGCGTGCTACTACTCACG 615	
λ ₀ λ	760		
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ь В 9	820	ASCTICACGARITCIGAIANTAIAGTCCCTGGAGTTAIGCAGCTAATTAAAGGTCAA 879	
δy	880	92	
q	736	ATCCAACCTGCACCAGAGTTGTCCTTTGAAGGCACCAATCTGGAC 79	
Ха	922	ATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTATGCATATGCTGGTTGTTTAC 981	
qq	962	GIGGGGAACATTGTGTTGGCATTGTACAGTGGCCTCTTCGCCTACGGAGGATGGAACTAT 855	
λα qa	982	CTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAAACCATTCCCCTTGCAATATGT 1041 	н
ζ	1042	11	П
ą	916	ATCICCTIGCCCATGCACCCTGGTCTATGTGCTGACGAACCTGGCCTACTTCACTACC 975	
λά a	1102	ATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTA 1161	
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λ	1342	TTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGCCTCGACAGTCTTTTGAATTTC 1401	П
ą	1216	ACGIGIGATGACCTGATGIACCCTTCTCCAGAGACATCTTCTCCATCATCATC 1275	ω
λ̈́	1402	CTCAGITITGCCAGGIGGCITITIAITGGGCIGGCAGTIGCIGGGCTGAITTATCTICGA 1461	_

Search completed: April 16, 2003, 06:28:27 Job time : 533 secs

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                                                           292 GGAAGAGGCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAAAAGTGCAGCTGAAG 351
                                                                                                                                       352 AGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGA 411
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                                                                                                655 GGATCTGACACCAGCCCTGAGGCCGAGGCTAGCTCGGGAGGGGGCGGAGTAGCCCTGAAG 714
                    Gaps
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                    Indels
                  0; Mismatches 622;
    Pred. No. 3.1e-80;
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                    Matches 747; Conservative
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This sequence represents cDNA encoding a rat neutral amino acid transporter, LAT1. It interacts with a 528 amino acid protein (AAY58427) to effect neutral amino acid transport. LAT1 is predicted to have up to twelve transmembrane domains from hydropathy analysis. The protein, and nuclealc acids encoding it are useful for the in vitro analysis of
                                 1363 ATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTT 1422
                                                                  1735 ATGCTGGTCACCAGTGACATGTATACACTCCATCAACTACGTGGGCTTCATCAACTACCTC 1794
                                                                                                     ITTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCAT 1482
                                                                                                                           CGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATG 1542
                                                                                                                                                                                           GITGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTG 1602
1675 CACGTGAAGCGCTGCACCCCAATCCCAGCACTGCTCTTCACATGCCTCTCCACCTGCTG 1734
                                                                                                                                                                                                                                                                          1915 CTGATTTTCAGCCTGTGGTCAGAGCCAGTAGTATGCGGCATTGGCCTTGCCATCATGCTG 1974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug permeation through cell membranes and blood tissue barriers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 15.4%; Score 343.8; DB 21; Length 1632; Best Local Similarity 54.4%; Pred. No. 3.6e-80; Matches 727; Conservative 0; Mismatches 592; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Neutral amino acid transporter LAT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat; neutral amino acid transporter; LAT1; drug permeation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1632 BP; 280 A; 504 C; 473 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA encoding rat neutral amino acid transporter LAT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A neutral amino acid transporter and its gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 10-13; 17pp; Japanese.
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64..1602
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                                         DB 22; Length 4585;
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           Sequence 4585 BP; 794 A; 1475 C; 1303 G; 1013 T; 0 other;
                                                                    Indels
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Pred. No. 1.6e-82;
0; Mismatches 589;
                                        15.8%;
55.2%;
                                                                 Matches 736; Conservative
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substrate selectivity to neutral amino acids, and which is inactivated by an amino acid transport activating factor 4F2hc (4F2 heavy chain). The neutral amino acid transporter and its gene are useful in in vitro analysis of permeation of drugs and poisons through cell membrane, blood and tissues. The present sequence represents cDNA encoding the rat L-type amino acid transporter 2 (LAT2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A neutral amino acid transporter having broad substrate selectivity useful for in vitro analysis of permeation of drugs and poisons through cell membranes, blood and tissues -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neutral amino acid transporter; amino acid transport activating factor; 4F2hc; 4F2 heavy chain; drug permeation; poison; rat; LAT2; L-type amino acid transporter 2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a neutral amino acid transporter having broad
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                                                                                                          TCACATGCCTCTTCATGGTTGCCCTTTCCCTCT---ATTCGGACCCATTTAGTACAGGGA 1582
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                                                           1207 GTGTGATGACGCTGTTTTACGCCTTCTCCAAGGACATCTTCTCGGTCATCAACTTCTTCA 1266
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                                                                                        1406 GITITGCCAGGTGGCTTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACA
                                                                                                                                                     1466 AATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat cDNA encoding L-type amino acid transporter 2 (LAT2).
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P-PSDB; AAB72393.
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DB 22; Length 4117;

Score 344.8;

15.4%;

Query Match

Sequence 4117 BP; 920 A; 1206 C; 970 G; 1021 T; 0 other;

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Human; cytokine; cell proliferation; cell differentiation; growth factor;
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                                                                       872 AAGGTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGAAGAGATTCAAG-----TATTA 925
812 CCTTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTA 871
                                                                                                           662 AGGGUGAUGUGUCCAAUCUAGAUCCCAACUUCUCAUUUGAAGGCACCAAACUGGAUGUGG 721
                                 602 ccGccGcCAAGCUCCUGGCCCUGGCCCUGAUCAUCCUGCUGGGCUUCGUCCAGAUCGGGA 661
                                                                                                                                                                                                                                                                                                                                                                                                     902 CCACCGAGCAGAGGCUGUCGAGGCCGUGGCCGUGGACUUCGGGAACUAUCACCUGG
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1442 AGCCCAAGUGGCU 1454
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bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss. inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;

Homo sapiens.

WO200157188-A2.

39-AUG-2001.

05-FEB-2001; 2001WO-US03800.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC.

fang YT, Liu C,

WPI; 2001-457740/49. P-PSDB; ABB12114. Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer

Claim 1; Page 918-919; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides of the invention. Although novel, many of the polypeptides of the invention. Although novel, many of the polypeptides of the invention. Although novel, many of the polypeptides of the invention. The polypeptides of the invention are polypeptides of the invention. The polypeptides of the invention may differential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell differentiation activities, seem cell growth factor activities; chemotactic or chemokinetic activities; haemostatic, thrombolytic activities, receptor or ligand activities, or may be used in oncogenesis, receptor or ligand activities, or may be conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, proliferation for nucleic acids encoding them) may be used to promodulatory activities may be used in the treatment of viral, and almondulatory activities may be used in the treatment of viral, and almondulatory activities may be used in the treatment of viral, may be used in the used to any be used to any be used in the readers of the used to any be used in the readers of the anyment of a very of promote cell growth. For example, or all seases, and the properties an that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a CDNA encoding a novel human polypeptide of the invention.

haematopoiesis regulation; tissue growth; immunomodulator; activin;

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1140 AGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGC 1199
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The present invention describes a cell surface protein which is an L-type amino acid transporter-1 (LATI), which mediates the transport of neutral amino acids, leucine, isoleucine, phenylalanine, methionine, tyrosine, tryptophan, value and histidine, into the cell independently of sodium ions. The LATI protein conjugates with the cell membrane surface molecule 4F2. Antisense DNA or RNA, antibodies, antibodos fragments, and peptide and non-peptide antagonists to IATI are useful as anticancer agents. The present sequence encodes human LATI, which is specifically claimed in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1524 BP; 245 A; 516 C; 438 G; 325 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 176-180; 189pp; Japanese.
                                                                                                                                                                                              (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                             99WO-JP04789
                                                                                                                                            98JP-0249993.
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P-PSDB; AAY82488.
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               Homo sapiens.
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                                                                                        912 GAACCTGCCCTCTCCATTGCCATCTCCATGCCCATTGTCACCATCATCTTGAC
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prevention of cancer e.g. adenocarcinoma, lung cancer, ovarian cancer, inflammatory/autoimmune disorders e.g. AIDS, Crohn's disease, rheumatoid arthritis; and cell proliferation disorders e.g. arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence encodes a human amino acid permease homologue (AAPH). The
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                                                                                                                                                                                                                                                                                                                                                                             New human amino acid permease homolog (AAPH) polynucleotide and its complement useful for prevention and treatment of cancer, autoimmune
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/product= "amino acid permease homologue (AAPH)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 366.4; DB 20; Length 2072;
Pred. No. 4.4e-86;
0; Mismatches 606; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2072 BP; 446 A; 537 C; 494 G; 595 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 1A-F; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      and cell proliferation disorders
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54.68;
                                                                                                                                   98US-0073362
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Best Local Similarity 54.69
Matches 730; Conservative
                                                                                                                                                                                                                          (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                   Hillman JL,
                                                                                                                                                                                                                                                                                                               WPI; 1999-493508/41.
                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY27076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic sequence.
                                                                                                                                   06-MAY-1998;
                                                                                                                                                                              J6-MAY-1998;
                                           US5942399-A
                                                                                                                                                                                                                                                                      Corley NC,
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Amino acid permease homolog; AAPH; cancer; inflammatory disorder; AIDS; autolimune disorder; anemia; asthma; atherosolerosis; diabetes mellitus; multiple sclerosis; osteoarthritis; osteoporosis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferation disorder; human; ss.
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                                                                       1080 AAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGC 1139
816 GAACCTGCCCCTCTCCATTGGCATCTCCATGCCCATTGTCACCATCATCTATATCTTGAC
                                                                                                                                                                                                                              1140 AGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ23240 standard; cDNA; 2072 BP
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runs cund amino acid permease nomblo (AARPH)

uncleic acid, protein, AAPH (ant)agonists are useful in the diagnosis, treatment and prevention of cancer such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymns, thyroid or uterus; inflammatory/autoimmune disorders such as AIDS, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthoroscalerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, cholecystitis, dermatomyosistis, mellitus, crohn's disease, atopic dermatitis, dermatomyosistis, emphysema, multiple sclerosis, osteoarthritis, osteoporosis, rheumatoid protozoal infections; and cell proliferation disorders such as actinic, beautosis, crirhosis, arteriosclerosis, myelofibrosis, and primary
                                                                                                                                                                                CDNA encodes a human amino acid permease homolog (AAPH). The AAPH
                                                         treatment and prevention of cancer, inflammatory/autolmmune disorders and cell proliferation disorders
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                                           New human amino acid permease homolog, useful in the diagnosis,
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                                                                                                                                   Disclosure; Fig 1A-F; 32pp; English.
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Matches 730; Conserv
P-PSDB; AAY41159
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                                                                                                                              TGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACAC 1319
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                                                                                                                                                                                                                                                                     IGCIGGGCIGATITAICTICGATACAAAIGCCCAGATAIGCAICGICCITICAAGGIGCC 1499
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1; monp-2; cell proliferation; drug development; immune disease; development; cancer; ss.
                                                                                                                                                                                                                        CCTCGACAGTCTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTATTGGGCTGGCAGT
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This invention describes a novel protein MONP-2 (I) and its encoding gene monp-2 (II) with a cell proliferation promoting effect isolated from a human peripheral blood. The new protein (I) and gene are useful in studying the expression abnormality and dysfunction of (I) as well as maintenance of immune function and development of drugs for e.g. immune diseases and cancers. This sequence encodes the MONP-2 protein described in the method of the invention.
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1106 ATGCTGAGGAGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGG 1165
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This invention describes a novel protein MONP-2 (I) and its encoding gene monp-2 (II) with a cell proliferation promoting effect isolated from a human peripheral blood. The new protein (I) and gene are useful in studying the expression abnormality and dysfunction of (I) as well as maintenance of immune function and development of drugs for e.g. immune diseases and cancers. This sequence encodes the MONP-2 protein described in the method of the invention.
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proliferation promoting effect, useful in studying its expression immune function, and in developing drugs for e.g. immune diseases
                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 1533;
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                                                                                                                                                                                                                                                                                                                                    Sequence 1533 BP; 301 A; 420 C; 363 G; 448 T; 1 other;
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16.4%; Score 366.4; DB 21;
Best Local Similarity 54.6%; Pred. No. 3.8e-86;
Matches 730; Conservative 0; Mismatches 606;
                                                                                                   Claim 3; Page 26-27; 34pp; Japanese
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                                                                                                                  TCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGT 1340
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613 TACTCAAGGTTGCCAGGTGGCTTTTTATTGGGCTGGCAATTGCTGGGCTTGATTTATCTT 672
                                                                                                                                                                                                                                                         673 NGAINCAAAIGCCNANATAIGCAICGGICCCTITCAAAGGIGCCCCTGIICAILLIIII | 132
                                                                                     TITGCACCCITTGACAATGATAATGCTCTTCTT-GGAGACCTCGACAGTCTTTGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                        Human L-type amino acid transporter 1 nucleotide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                           L-type amino acid transporter 1; LAT1; 4F2hc; 4F2 heavy chain; neutral amino acid transporter; tumour; cancer; proliferation; cell membrane surface 4F2 molecule; anticancer; ss.
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The present invention describes a cell surface protein which is an L-type amino acid transporter-1 (LAT1), which mediates the transport of neutral amino acids, leucine, isoleucine, phenylalanine, methionine, tyrosine, tryptophan, value and histidine, into the cell independently of sodium ions. The LAT1 protein conjugates with the cell membrane surface molecule 4F2. Antisense DNA or RNA, antibodies, antibody fragments, and peptide and non-peptide antagonists to LAT1 are useful as anticancer agents. The present sequence encodes human LAT1, which is specifically claimed in the present invention.
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Neutral amino acid transporter protein which conjugates with cell membrane protein 4F2 and operates independently of sodium ions is useful for screening potential cancer proliferation inhibitors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 TYCCNACCTGCCCGGTGCCCGAGGAGGCAGCCAAGCTCGTGGCCTGYYINTGYGTGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 4539;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4539 BP; 765 A; 1450 C; 1297 G; 998 T; 29 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 16.6%; Score 370.8; DB 21; Length Best Local Similarity 54.4%; Pred. No. 4.5e-87; Matches 725; Conservative 13; Mismatches 589; Indels
                                                                                             Claim 9; Page 125-132; 189pp; Japanese.
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                                                                                                                                                                                                                                                                     TTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCCAGATATGCATC 1483
1184 TICCGAICTITGITGCCCTCTCCTGCTITGGCTCCATGAACGGTGGTGTTTTGCTGTCT 1243
                                                                                                                                                                              1304 AIGICCGCAAGCACACTCCICTACCAGCTGTTAITGTTTTGCACCCITTGACAAIGATAA 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITCAAAIGCAGIGGCAGIGACCIITICIGAGCGGCIACIGGGAAAITICICAIIAGCAG 1183
                                                                                                                                   1244 CCAGGITATICTATGTIGCGICTCGAGAGGGICACCTICCAGAAAICCTCCTCCATGATIC 1303
                                                                                                                                                                                                                                                                                                                                                                                                                   355 TGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTT 414
                                                                                                                                                                                                                                                                                   Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                       Human gene expression product cDNA sequence SEQ ID NO:4565.
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The present invention describes a library of human polynucleotides

C comprising the sequences given in AAZ12532 to AAZ1779. Also described is

C comperious state of a mammalian cell, comprising detecting at least one

cancerous state of a mammalian cell, comprising detecting at least one

differentially expressed gene product in a test sample from a cell

cuspected of being cancerous, where the gene product is encoded by one

CC the 5148 polynucleotide sequences given in AAZ12532 to AAZ17779. The

cof the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The

cof the 518 polynucleotide sequences of primers and probes, which can

compaping, tissue typing or profiling, forensics, genetic analysis and

detection of polymorphisms. Polypeptides encoded by the polynucleotides

cc antengentic purposes. The polynucleotides may also be used to construct

therapeutic purposes. The polynucleotides may also be used to construct

cc arrays for diagnostics (which may be used to determine function of an

encoded protein); and to detect differences in expression levels between

two cells (e.g. to identify abnormal or diseased tissue in a human, to

two cells (e.g. to identify abnormal or diseased tissue in a human, to

two cells, prognosis and management of colorectal cancer, breast cancer,

and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1105 AATGCTGAGGAGCTGCTGTTCAAATGCA-GTGGCAGTGACCTTTTCTGAGCGGCTACT 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       985 AACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAAACCATTCCCCTTGCAATATGTATA 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    865 CTAATTAAAGGTCAAAACGCAGAACTTTAAAGACGCCTTTTCAGGAAGAGATTCAAGTATT 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 520.6; DB 20; Length 761;
Pred. No. 5.6e-127;
0; Mismatches 72; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reinhard C;
                                                                                                                                                                                                                                                                                                                                                         Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 761 BP; 160 A; 162 C; 150 G; 250 T; 39 other;
                                                                                                                                                                                                                          Innis MA;
                                                                                                                                                                                                       Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Szcobedo J, Garcia PD, Garcia W, Giese K, Innis l
Jones WL, Kasam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinh
                                                                                                                                                                                                                                                                            Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2164-2165; 2479pp; English.
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88.2%;
                                                    98US-0072910.
98US-0075954.
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99WO-US01619
                                    9990800-Sn86
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                                                                                                                                                   CHIR ) CHIRON CORP.
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                                                                                                                                                                         (HYSE-) HYSEQ INC.
28-JAN-1999;
                                                        28-JAN-1998;
24-FEB-1998;
                                                                                          31-MAR-1998;
03-APR-1998;
                                      03-APR-1998;
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GIGCIGACAAAIGIGGCCTACTITACGACCATTAAIGCIGAGGAGCIGCIGCITICAAAI 1131
                                       1132 GCAGTGGCAGTGACCTTTTCTGAGCGCCTACTGGGAAATTTCTCATTAGCAGTTCCGATC 1191
                                                    1192 TITGTIGCCCTCTCCTGCTTIGGCTCCATGAACGGIGGIGTTIGCTGTCTCCAGGITA 1251
                                                                                           1252 ITCTATGTTGCGTCTCGAGAGGTCACCTTCCAGAATCCTCTCCATGATTCATGTCCGC 1311
                                                                                                                                    1312 AAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTC 1371
                                                                                                                                                                             1372 TCIGGAGACCICGACAGICTTITGAATTICCICAGTITIGCCAGGIGGCTTITIATIGGG 1431
                                                                                                                                                                                                                     CIGGCAGTIGCIGGGCIGATITAICTICGAIACAAAIGCCCAGAIAIGCAICGICCITIC 1491
                                                                                                                                                                                                                                                              1492 AAGGIGCCACIGTICATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTT 1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1852 ITATITITATICATATATITTAGCATATICGAACTAATTTCTAAGAAATITAGTIATAAC 1911
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The present invention describes a library of human polynucleotides

C comprising the sequences given in AA212532 to AA21779. Also described is comprising the sequences given in AA212532 to AA21779. Also described is a method of detecting all terantially expressed gene product in a test sample from a cell of differentially expressed gene product in a test sample from a cell of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AA212532 to AA21779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profilling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between the construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between the construct and to detect differences in expression levels between the construct and the detect differences in expression levels between the construct and the detect of the construct and the constr
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                                                                                                                                                                                                                                                                              Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                            Human gene expression product cDNA sequence SEQ ID NO:3998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human genes and their expression products which are differentially expressed in different cell types
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1897; 2479pp; English.
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                                                        AAZ16528 standard; cDNA; 772 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0080666.
98US-0072910.
98US-0075954.
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98US-0080515.
                                                                                                                                                                      12-OCT-1999 (first entry)
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24-FEB-1998;
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03-APR-1998;
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                                                                                                                 AAZ16528;
RESULT 5
AAZ16528
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9

6; Gaps

5; Indels

0; Mismatches

Conservative

Similarity

Query Match Best Local Simi Matches 711;

28.8%; Score 643.8; DB 20; Length 772; 98.5%; Pred. No. 1.8e-159;

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forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                       Sequence 1958 BP; 499 A; 418 C; 424 G; 617 T; 0 other;
                                  of the invention.
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                                                                                                                                                                                                                                                                                     1686 TTATTTTATTCATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAAC 1745
                                                                                                                                                                     1972 TCTGATACCTACTACCTATTGGGGTTAGGAAAAAGACTAGACAATTACTATGTGGTCATTCT 2031
                                                                                                                                                                                                                                         1806 TCTGATACCTACTTGGGGTTAGGAGAAAAGACTAGACAATTACTATGTGGTCATTCT 1865
                                                                                                                                                                                                                                                                     CTACAACATATGTTAGCACGGCAAAGAACCTTCAAATTGAAGACTGAGATTTTTCTGTAT 2091
         1566 TGAACTAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATTT 1625
                                                                 1626 TTACTTCATTTTCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAAACAAAAGGAGTCAG 1685
                                                                                            1852 TTATTTTTATTCATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAAC 1911
                                                                                                                                                    1912 TCTATGTAGTTATAGAAAGTGAATATGCAGTTATTCTATGAGTCGCACAATTCTTGAGTC 1971
                                     1792 TTACTICATTITCIGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAAGGAGTCAG 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang Z, Chen R, Asundi V;
                                                                                                                                                                                                                             Human EST-derived coding sequence SEQ ID NO: 430.
                                                                                                                                                                                                                                                                                                                                               1926 ATATGGGTTTTGGAAGATGGTTTTACACACTA 1958
                                                                                                                                                                                                                                                                                                                                 2092 ATATGGGTTTTGTAAAGATGGTTTTACACACTA 2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Liu C, Zhou P, Qian XB, Wang
Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 484; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH98573 standard; cDNA; 1958 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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AAH98573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 ATGAGTGTCAGCTGGAGCGCCGGATCCAGATTTCTTAACCTTTTGCAGAGCTCACAGG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 606 AIGAGIGICAGCIGGAGCGCCCGGAICCAGAITITCITAACCTITIGCAAGCICACAGCA 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             832 ATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTT 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGACGCCTTTTCAGGAAGAGTTCAAGTATTACGCGGGTTGCCACTGGCTTTTTATTAT 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 ACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGTCCATTA 591
                                                                                                                                                                                                                                                      292 GGAAGAGACGCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAG 351
                                                                                                                                                                                                                                                                                                                  352 AGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGA 411
                                                                                                                                                                                                                                                                                                                                                                                                 531
                                                                                                                            172 CTGGATTCAGGAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAAT 231
                                                                                                                                              232 GTTAACGGGAGGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCA 291
                                                                                                                                                                                                                                                                                                                                                                                  471
                                                               112 CAATTGTGGCATAGATTTTATCATATTCTGGATTTTTGGATTCTTTTGTTTTTCTCATCA 171
                                                                                            1 caaiiccceesiceaceaiiiceiiiiccicigiiiiariiiicccccesesiciccia 60
                                    Gaps
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                                                                                                                                                                                                          168 -----GAGAAAGIGCAGCIGAAG
                                                                                                                                                                                                                                                                                                                                   412 ATCTTCATCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACC
Query Match
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1920; Conservative 0; Mismatches 38; Indels 55;
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c giving an insight into their probable biological activities, and hence becential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell aematopolesis regulatory activity; tissue growth activity; immunomodulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinelic activities; haemostatic, thrombotic or chemokinelic activities; haemostatic, thrombotic or proposed in oncogenesis, cancer cell proliferation or metastasis. thrombolytic activities; receptor or ligand activities; or may be pepending on their biological activities, polypeptides and nucleotides of conditions, e.g., by protein or preventing, treating or ameliorating medical cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal cy ascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound immunomodulatory activities may be used in the treatment of viral, conventides with arrowth fartor arrivity may be used in chart or mucle. Conventivity may be used in the properties of polyperides with marowth fartor arrivity may be used in the invention or includent to a promoter or material and fungal infections in addition to immune disorders. autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, screening techniques. The present sequence novel human polypeptide of the invention.

Sequence 1958 BP; 499 A; 418 C; 424 G; 617 T; 0 other;

5 CAATTGTGGCATAGATTTTATCATATTCTGGATTTTTTGGATTCTTTTGTTTTCTCATCA 171 GTTAACGGGAGGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGGCAGGACGCCTTTTCA 291 168 -----GAGAAAGTGCAGCTGAAG 185 172 CTGGATTCAGGAAAGCCTGTTGTGTCCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAAT 231 120 GTTAACGGGAGGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAG------ 167 292 GGAAGAGACGCCTTTTCAGGAAGACGCCTTTTCAGGAAGAGAAAAGTGCAGCTGAAG 351 352 AGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGA 411 55; Gaps 1 CAATICCCGGGICGACGAITICGITITICCCTCIGITITATITITCCCCCGIGGICCCCIA 60 412 ATCTTCATCTCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACC 471 ATCTGGACGGTGTGGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGA 531 ArcidGACGGTGTGTGGGGTCCTGTCATTTGGAGCTTTGTTTATGCTGAATTGGGA 365 ACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGTCCATTA 591 366 ACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGTCCATTA 425 592 CCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTG 651 652 ATATCCCIGGCATTIGGACGCIACATICIGGAACCATTITITATICAATGIGAAATCCCT 711 DB 22; Length 1958; 0; Mismatches 38; Indels 81.4%; Score 1822.2; 95.4%; Pred. No. 0; Matches 1920; Conservative Similarity Query Match 112 232 472 306 532 g ò ò 윤 δ 셤 ŏ Q δy g ò q g ŏ g ò ð g δ

952 GGAATGTATGCATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAC 1011 1012 CCTGAAAAACCATTCCCCTTGCAATATGTATCCATGGCCATTGTCACCATTGGCTAT 1071 486 ATATCCCIGGCATTIGGACGCTACATICTGGAACCATTITITITITATCAATGTGAAATCCCT 545 1072 GTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAAT 1131 712 GAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGC 771 772 ATGAGTGTCAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCA 831 1192 TITGITGCCCICTCCTGCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTCCCAGGTTA 1251 1252 TICIATGITGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGC 1311 1312 AAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTC 1371 1146 AAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCTTTGACAATGATAATGCTCTTC 1205 1372 TCTGGAGACCTCGACAGTCTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTATTGGG 1431 1206 TCTGGAGACCTCGACAGTCTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTATTGGG 1265 891 725 951 1491 1266 CTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATGTCTTC 1325 1492 AAGGIGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTT 1551 1552 TCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTC 1611 1386 TCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTC 1445 1612 CCTGCGTATTATCTCTTTATTATGGGACAAGAAACCCAGGTGGTTTAGAATATGTCA 1671 1446 CCTGCGTATTATCTTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCA 1505 GAGAAAATAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAAGAAGATAAGTTA 1731 1732 IGAACTAATGGACTIGAGAICTIGGCAATCIGGCCAAGGGGAGACACAAAATAGGGAITT 1791 832 ATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTT 666 ATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTT 892 AAAGACGCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTAT 846 CCTGAAAAAACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTAT 1132 GCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATC 906 GIGCIGACAAATGIGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGTTTCAAAT 1432 CIGGCAGTIGCIGGCCIGATITAICTICGATACAAIGCCCCAGAIAIGCAICGICCTITC δλ q ŏ qq ŏλ qq QQ δ Qγ gg δλ qq δŏ g δ q δλ Q δy qq όλ QQ ŏ δ Db Óγ q δλ δ Dp

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1747 TCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAAGGAGTCAGTTATTTTATT 1806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGACCT 1382
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                                                                                                                                                                                                                                                                                                                               GTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCC 1322
                                                                                                         CATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAA 1082
                                                                                                                         1083 TGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTCAAATGCAGTGGCAGT 1142
                                                                                                                                                                             1027 TGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGT 1086
                                                                                                                                                                                                                      1202
                                                   ATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCTGAAAAAC 1022
1687 ACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAAATAGGGATTTTTACTTCATTT
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                                                                                                                                                                                                                    GACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCT
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haematopolesis regulation; tissue growth; immunomodulator; activit; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; caener; tumnour; haematopoletic disorder; proliferation; metastasis; caener; tumnour; haematopoletic disorder; proliferative retinopath; chronic inflammatory condition; proliferative retinopath; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell outlure; drug screening; gene therapy; antiinflammatory; antiarthritic; haemostatic; antiarteriosclerotic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiuloer; ss.
                                                                                                                                                                  2103 GTAAAGATGGTTTTACACACTACAGATGTCTATACTGTGAAAAGTGTTTTCAATTCTGAA 2162
1983 CCTATTGGGGTTAGGAGAAAAGACTAGACAATTACTATGTGGTCATTCTCTACAACATAT 2042
                   Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                         2043 GTTAGCACGGCAAAGAACCTTCAAATTGAAGACTGAGATTTTCTGTATATATGGGTTTT
                                                                                            Human cystine/Glu transporter homologue cDNA, SEQ ID NO:977.
                                                                                                                                                                                                                                         2163 AAAAAGCATACATGATTATGGCAAAGAGGAGGAAGGTA 2204
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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P-PSDB; ABB11957.
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1801 TITCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAAGGAGTCAGTTATTTTA 1860
                       1861 TICATATATITITAGCATATITGGAACTAATTITCTAAGAAATTITAGTTATAACTCTATGTAG 1920
                                   1921 TTATAGAAAGTGAATATGCAGTTATTCTATGAGTCGCACAATTCTTGAGTCTCTGATACC 1980
                                                                                 1981 TACCTATTGGGGTTAGGAGAAAAGGACTAGACAATTACTATGTGGGTCATTCTCTACAACAT 2040
                                                                                                                                                                           TTGTAAAGATGGTTTTACACACTACAGATGTCTATACTGTGAAAAGTGTTTTCAATTCTG 2160
                                                                                                                                                                                                                      2161 AAAAAAAGCATACATCATGATTATGGCAAAGAGGAGAAAGGTAGAGCTGTTCTTAAATT 2220
                                                                                                                                                                                                                                                                   protein; immunostimulant; cytostatic; gene therapy;
Vaccine; immune response; lung cancer; 14F10; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and
                                                                                                                              2041 AIGITAGCACGGCAAAGAACCTICAAATTGAAGACTGAGATTTTTCTGTATATATGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human lung-specific polynucleotides and polypeptides for the diagnosis and treatment of disease e.g. lung cancer -
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PA, Elliot M, Mannion J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lung tumour-specific 14F10 full length cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 332-334; 378pp; English.
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Fling SP, Algate PA,
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2000US-0640878.
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                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; lung tumour
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14-DEC-2000;
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expanding T cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition useful for stimulating an immune response, and for treating cancer. The lung tumour specific oligonocleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence is a cDNA encoding human lung tumour-specific protein.
                                                                                                                                                                                                                                                                     63 AATTAAGGAAAAAAAAAAAAAAAAAAAAAGAGAGGAAATTCCAGGCCAATTGTGGGA 122
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antigen-presenting cells are useful for stimulating and/or
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                                                                                                                   Sequence 5981 BP; 1858 A; 1029 C; 1098 G; 1996 T; 0 other;
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0; Mismatches
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Matches 2146; Conservative
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WPI; 2001-639201/73.

New human lung-specific polynucleotides and polypeptides for the diagnosis and treatment of disease e.g. lung cancer –

Claim 1; Page 332; 378pp; English

their corresponding cDNA molecules. Lung tunnour-specific proteins and their corresponding cDNA molecules. Lung tunnour specific proteins and their antiqen-presenting cells are useful for stimulating and/or expanding rells specific for a tunnour protein, and for inhibiting the development of cancer The invention also relates to a composition useful for stimulating an immune response, and for treating cancer. The lung tunnour specific oligonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence a cDNA encoding human lung tumour-specific protein.

Sequence 2239 BP; 619 A; 444 C; 493 G; 683 T; 0 other;

ö Gaps DB 23; Length 2239; .; 0 0; Indels 0; Mismatches 100.0%; Score 2239; 100.0%; Pred. No. 0; Matches 2239; Conservative Similarity Query Match

1 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAC 60 ð

1 GGAGGITGAAGTGAGCAGGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAC

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241 AGGTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAAC 300

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GTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATA 540 GTGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATA 540 421 481 481 염 음 ò

GTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGTATCCCTG ŏ g ò

541 AAGAAATCIGGAGGICATIACACAIATATITIGGAAGICITIGGICCAITACCAGCIIII 600

661 GCATTIGGACGCTACATICTGGAACCATTITTATTCAATGTGAAATCCCTGAACTTGCG 720 GCATITIGGACGCTACATICIGGAACCATITITITATICAATGTGAAATCCCTGAACTIGCG 720 g qq ò

721 AICAAGCICAITACAGCIGIGGGCAIAACIGIAGIGAIGGICCIAAAIAGCAIGAGIGIC 780

661

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1801 TITCIGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAAGGAGTCAGTTATTTTA 1860 1741 GGACTTGAGATCTTGGCAATCTGCCCCAAGGGGAGACACAAAATAGGGATTTTTACTTCAT 1800 1741 GGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATTTTTACTTCAT 1800 1681 ACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAAGATAAGTTATGAACTAAT 1740 1501 CIGIICAICCCAGCITIGIITITCCITCACAIGCCICITCAIGGIIGCCCITICCCICIAI 1560 1561 TCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTAT 1620 1621 TATCTCTTTATTATATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATA 1680 CTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTTATTGGGCTGGCAGTT 1440 1441 GCTGGGCTGATTTATCTTCGATACAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCA 1500 GCGTCTCGAGAGGGTCACCTTCCAGAATCCTCTCCATGATTCATGTCCGCAAGCACACT 1320 1081 AAIGIGGCCIACITIACGACCAITAAIGCIGAGGAGCIGCIGCTITCAAAIGCAGIGGCA 1140 1141 GIGACCITITICIGAGCGGCTACIGGGAAATTICICAITAGCAGTICCGAICITIGIIGCC 1200 961 GCATATGCTGGCTGGTTTTACCTCAACTTGTTACTGAAGAAGTAGAAAACCCTGAAAAA 1020 961 GCATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAA 1020 781 AĞCTGGAĞCGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATA 840 CICICCIGCITIGGCICCAIGAACGGIGGIGITITGCIGICICCCAGGITAIICIAIGII GCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCCTGCATGATTCATGTCCGCAAGCACACT TTTTCAGGAAGAATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTAT ATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAAGACGCC 1381 1201 1201 1261 1261 QQ ò δ g δ g g ò g g g ò q Ω ò g δλ g δ Qγ g g δλ ò g Ω g ò ò Qγ

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GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Human lung timoning	ThOIR 6	Human lung tumour-	Human cystine/Glu	Human EST-derived	Human gene express	Human gene express	Human L-type amino	Human monn-2 chna	Human mono-2 chan	131777 a J
SUMMARIES		ID		AAD23460	AAD23461	ABA00201	TO TO TO TO	AAR16500	AA610066	AA21/094	AAAU03/2	AAA11934	AAA11955	
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16.4 2072 16.8 16.85 15.8 4585 15.4 4117 15.4 4117 15.4 42155 15.4 42155 15.4 42155 15.4 42151 15.4 42151 15.4 42151 15.4 4215 16.4 2155 14.7 2090 14.5 1997 14.1 1918 13.9 1918 13.4 300 13.4 300 12.9 300 12.9 300 12.6 3984 10.6 3984 10.6 3984 10.1 2564	0.4.
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ALIGNMENTS

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AAD23460
ID AAD23460 standard; CDNA; 2239 BP.

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AAD23460;
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AAD23460;
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AAD23460;
XX
B Human lung tumour-specific 19A4 CDNA.

XX
Human lung tumour protein; immunostimulant; cytostatic; gene therapy; XX
Antisense-therapy; vaccine; immune response; lung cancer; 19A4; ss.

XX
Homo sapiens.

XX
Homo sapiens.

XX
PN
WO200172295-A2.

PN
WO200172295-A2.

PN
YX
PR
29-MAR-2001; 2001W0-US09991.

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PR
29-MAR-2000; 2000US-058837.
PR
18-4UG-2000; 2000US-0640873.
PR
18-AUG-2000; 2000US-0640873.
PR
14-DEC-2000; 2000US-0738973.
PR
14-DEC-2000; 2000US-0738973.
PR
14-DEC-2000; 2000US-0738973.

XX
Reed SG, Lodes MJ, Mohamath R, Secrist H, Benson DR, Indirias CY; PI Henderson RA, Filing SP, Algate PA, Elliot M, Mannion J, Kalos MD;
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924 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8033076 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6091235
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 924)
242 GGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACG 301
                                    198 GCTCCCTCCGTGGGGACCAAGAGCCACCTGGGCAT---------235
                                                                    302 CCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAAAAGTGCAGCTGAAGAGGAAAGTCA 361
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                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NIH_MGC_112"
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Location/Qualifiers
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157

BASE COUNT

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963 ATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCTGAAAAAAC 1022
                                                                                                                                                                                                                                                                                                                                                                                                                    1023 CATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAA 1082
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                                                                                789 CGCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATAATTATAGT 848
                                                                                                                                                                849 CCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTT-----TAAAGACGCCTT 902
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                                                                                                                                                                                                          62 GCTGGGCTTCGTCCAGATCGGGAAGGGTGATGTGTCCAATCTAGATCCCAACTTCTCATT 121
                                                                                                                                                                                                                                                    903 TICAGGAAGAGATICAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGTATGC 962
                                                                                                                                                                                                                                                                                          122 TGAAGGCACCAAACTGGATGTGGGGAACATTGTGCTGGCATTATACAGCGGCCTCTTTGC 181
                                                                                                                                                                                                                                                                                                                                                                            182 CTATGGAGGATGGAATTACTTGAATTTCGTCACAGGGAAATGATCAACCCCTACAGAAA 241
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                                                                                                                     2 CACCGGGTCCAGGATGCCTTTGCCGCCCAAGCTCCTGGCCCTGGCCCTGATCATCCT 61
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                                          0; Mismatches 374; Indels
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                 Best Local Similarity 54.9%
Matches 463; Conservative
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/clo
                        Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/TPP

CDNA Library Preparation: Run A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

Plate: LLCM2454 row: k column: 23

High quality sequence stop: 690.
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Unpublished (1999)
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combination of ROV, RBR, RKI, RLI, RPL, RLU, REM, RMU, RSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear EST 28-NOV-2000
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Malek, R.L., Cho, J., Lee, Y., Karamycheva, S., Parvizi, B., Pertea, G., Sultana, R., Tsai, J., White, J., Quackenbush, J. and Lee, N. H.
Seneration of ESTs from Normalized Rat Embryo, Bento Soares
Unpublished (2000)
Other_ESTs: EST450642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      524 bp mRNA linear EST 28-NOV-20 EST450643 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIFL83, mRNA sequence. BF286052
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                                                                                                                                                                                                                            1503 GTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTATTC 1562
                                            1383 CGACAGTCTTTTGAATTTCCTCAGTTTTTGCCAGGTGGCTTTTTATTGGGCTGGCAGTTGC 1442
                                                                                                                                       1443 TGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACT 1502
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                                                                                                                                                               602 CTTCTCCGTCATCAACTTCTTCAGCTTCTTCAACTGGCTTGGCCCTGGCCATCAT 661
542 CGTGCCGTCCTCGTGTTCACGTGTGATGACGCTGCTCTACGCCTTCTCCAAGGACAT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Rat Gene Index, normalized rat, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nhieetigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712, Medical Center Drive, Rockville, MD 20850, USA
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                          1623 TCTCTTTATTATGGGACAAGAAACCC 1650
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Fax: (301)-838-0208
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BQ430089
AGENCOURT_7809471 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6053290
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/tab_host="epithelioid carcinoma"
/tab_host="bH10B (phage-resistant)".
/note="Organ: pancras; Vector: pCNV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.1 kb. Library constructed by Life
Technologies "
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                      1039 TGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAATGTGGCCTACTTTACG 1098
                                                                                                                         1099 ACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGG 1158
                                                                                                                                                                                            1159 CTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCC 1218
                                                                                                                                                                                                                                                               1219 ATGAACGGTG-TGTTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCA 1277
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arcc
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 GCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGCACCATCAT 401
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                                                                                                                                                                                                                                                                                                                                1278 CCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCAC 1317
                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov Plate: LLAM13310 row: b column: 11
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/db_xref="taxon:9606"
/clone="IMAGE:6053290"
/clone_lib="NIH_MGC_70"
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 945)
402 TGGAGCAGGAATCTTCATCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCAT 461
                                                                         522 TGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTT 581
                                                                                                                                                                                                                                                                                                                                                                                 180 AGAGCIGGGACCACCATCACCAAGICGGGAGCCAGCIACGCITAIAITCIAGAGGCCIT 239
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                  462 GTCTCTGACCATCTGGACGGTGTGTGGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGC
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                                          334 GAGAAAGIGCAGCIGAAGAAGAGAAAGICACITIACIGAGGGGAGICICCAITAICAIIGGC 393
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(Wellome/CR Institute).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                  1465 AAATGCCCAGATATGCATGGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTCC 1524
1405 AGTITIGCCAGGIGGCTITITIAITGGGCIGGCAGITGCIGGGCIGAITIAICTICGAIAC 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                               1645 AAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAAC 1682
                                                                                                                                                                                                                                                                                                                                                                          Center For Genetic Resource Information
National Institute of Genetics
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/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed genes in X. laevis embryo Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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/clone="IMAGE:4796275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="embryonal carcinoma, cell line"
/lab_host="mbryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally; oligo-dr primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                               BG388107
602413070F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4521736 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                        NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAAGACG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 CCTTTTCAGGAAGAGGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 CTTTACTGAGGGG-AGTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 TCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 GTGTGTGGGGTCCTGTCACTATTTGGA-GCTTTGTCTTATGCTCAATTGGGAACAACTAT 539
                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 1072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.6%; Score 326.2; DB 12; Length 81.0%; Pred. No. 1.5e-52; Indels 1.0ve 0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 row: k column: 17
                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4521736"
/clone_lib="NIH_MGC_92"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop:
                                                                                                                                                                         BG388107.1 GI:13281553
                                                                                                                                                                                                                                                                                        (bases 1 to 1072)
 481 GATAGGCTCCCCTCCA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 477; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: LLAM10421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1072
                                                                                                                                       "RNA sequence.
                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                   Juman,
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                                                                                                               DEFINITION
                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                     ACCESSION
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                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                           RESULT 9
                                                                                                                                                                                         KEYWORDS
                                                                           BG388107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                         VERSION
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CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Pieror Carninci (RIKEN)

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www.shgc.stanford.edu

Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M. Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: e Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9790234
This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submitted (01-FEB-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                        599 ITGTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCC 658
                                                                                                                                                                                                             662 TCGTACGAGTATGGGTGGAACTCCTCATACTACGACTGACGCTACTGCTGTGATATCCC 721
                                                                                                                                                                                                                                                                                TGGCATTTGGACGCTACATTCTGGAACCATTTTTTTTTCAATGTGAAATCCCTGAACTTG 718
                                                                                                                                                                                                                                                                                                                            BC022457

1962 bp mRNA linear HTC 04-FEI Homo sapiens, solute carrier family 7, (cationic amino acid transporter, y+ system) member 10, clone IMAGE:4796275, mRNA.
540 AAAGAAATCIGGAGGTCATTACACA-TATATTTIGGAAGICTTIGGICCATTACCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 311.6; DB 11; Length 1962; Pred. No. 7.4e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                        719 CGATCAAGCTCAT-TACAGCTGTGGGCATAACTGTAGTGATGGTCCTAA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
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/clone_lib="NIH_MGC_96"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.9%;
52.9%;
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/note="Organ: placenta_normal; Vector: puc18; Site_1: Smal /note="Organ: placenta_normal; Vector: puc18; Site_1: Smal / Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196/716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti-PMO&t2-PMO-GNO344-
271200-001-f12&t3=2000-12-27&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1425 TATTGGG--CTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCAT 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1483 CGTCCTITCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATG 1542
                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1365 GCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTT 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1185 TCCGATCTTTGTTGCCCTCTTCCTTTGGCTCCATGAACGGTGGTGTTTGCTGTCTC 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1245 CAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCA 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1065 TGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCT 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 TAATGGGGCGTGGCAGATGCTGGGGTGATTTATCTTCGATACAAATGCCCAGATATGCAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1125 TICAAATGCAGTGGCAGTGACCTTTTCTGAGGGGCTACTGGGAAATTTCTCATTAGCAGT 1184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 rcaaaacccrcccrcccr--aaccirrcraccccraargccaaarrcrcaaraaccag 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%; Score 359.8; DB 14; Length 497; 88.1%; Pred. No. 7.6e-59; Live 0; Mismatches 52; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 t
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                          High quality sequence start: 106 High quality sequence stop: 117.
                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="GN0344"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                             Seq primer: puc 18 forward
                                                                                   Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1543 GTTGCCCTTTCCCTCTA 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 c
                                                                                                                                                                         Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                                                                                                 1 (bases 1 to 497)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, E., Garcia Correa, R., Zago, M.A., Bordin, S., Costa, F.F., Coldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B0370588 1inear EST 21-MAY-2002
PMO-GN0344-271200-001-f12 GN0344 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1901 TTAGTTATAACTCTATGTAGTTATAGAAAGTGAATATGCAGTTATTCTATGAGTCGCACA 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1781 AATAGGGATTTTTACTTCATTTTCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAACA 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1841 AAAGGAGTCAGTTATTTTTTTTTTTTTTAGCATATTTGGAACTAATTTCTAAGAAAT 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1721 AAGATAAGTTATGAACTAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAA 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 363; DB 14; Length 371; 98.6%; Pred. No. 2.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                   /clone_lib="Soares melanocyte 2NbHM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                               /organism="Homo sapiens"
/db_xref="GDB:3884033"
                                                                                 _xref="taxon:9606"
                                                                                                  /clone="IMAGE:290903"
             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ370588.1 GI:21046102
                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 363; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                     source
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BQ370588
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                      FEATURES
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/tissue_type="adenocarcinoma, cell line"
/tab_host="DH10B (phage-resistant)"
/note="Norgan: prostate; Vector: pCMV SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oiligo-dr primed.
Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602408645F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4537810 5',
                   378 CTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGCT 437
                                                                438 CCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGGTCCTGTC 497
                                                                                  498 ACTATITGGAGCTITGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCA 557
                                                                                                                                                      558 TTACACATATATTTTGGAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGA 617
                                                                                                                                                                                                                         618 ACTCCTCATAATACGCCCTGCAGCTACTGCTGATATCCCTGGCATTTGGACGCTACAT 677
                                                                                                                                                                                                                                                                                          678 TCTGGAACCATTTTTATTCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGC 737
                                                                                                                                                                                                                                                                                                                                                            NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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BG284503
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BG284503
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18.4%; Score 411.2; DB 12; Length 936;

Query Match

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1 (bases 1 to 371)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hullman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
R., Milliamson,A., Wooldman,P., Trevaskis,E., Waterston
R., Williamson,A., Wooldman,P., Tan,F., Trevaskis,E., Waterston
M., Williamson,A., Wooldman,P. and Wilson,R.
                                              182 GAAAGCUTGITGIGCCACCAICTCCAAAGGAGGITACCIGCAGGGAAAIGITAACGGGA 241
                                                               242 GGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACG 301
                                                                                                                              302 CCTTTTCAGGAAGACGCCTTTTCAGGAAGAGAAAGTGCAGCTGAAGAGAAAGTCA 361
                                                                                                                                                                                                           376 -----GAGAAAGTGCAGCTGAAGGTCA 403
                                                                                                                                                                                                                                                              362 CTTTACTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGAGGAGGAATCTTCATCT 421
                                                                                                                                                                                                                                                                                                                            422 CTCCTAAGGGGGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGG 481
                                                                                                                                                                                                                                                                                                                                                                          TGTGTGGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATAA 541
                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPrimer
High quality sequence stop: 339.
                       13; Indels 55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      542 AGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGTCCATTACCAGCTTTTG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661
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Y29612.rl Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:290903 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
   87.9%; Pred. No. 9.1e-69;
Live 0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                722 TCAAGCTCATTACAGCTGTGGG 743
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                  494; Conservative
Best Local Similarity
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EST 27-FEB-2001

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/tissue_type="renal call adenocarcinoma" /tissue_type="renal call adenocarcinoma" /lab_host="bH10B (phage-resistant)" /lab_host="bH10B (phage-resistant)" /lab_host="bH10B (phage-resistant)" /lab_host="bH10B (phage-resistant)" /lab_host="call" /lab_host="bH10B (phage-resistant)" /lab_host="call" /lab_host="call"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 910) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 CAACAAGGAGCCACCTGGGCAG------264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-rémail.nih.gov
Tissue procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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63 TTTTACTTCATTTTCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAA 10
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                                                                                                                                                                                  mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_14"
                                                                                                                                                                                  910 bp
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Matches 575; Conservative
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                                g
                  /note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The Not Is a subtracted library derived from Not_CGAP_Subl library, which is a subtracted library the Not_CGAP_Lord library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted Not_CGAP_Lord (NOT_CGAP_CO10).

NOT_CGAP_LOIG, NOT_CGAP_PY3B, NOT_CGAP_LOID, NOT_CGAP_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1610 TCCCTGCGTATTATCTCTTTATTATGGGACAAGAAACCCCAGGTGGTTTAGAATAATGT 1669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 472.4; DB 10; Length 483; Pred. No. 2.4e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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nes 473; Conservative
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1641	Lukatyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Bobort ctore.		/organism="Homo sapiens" /db_xref="taxon:9606" /db_xref="taxon:9606" /clone="InxoE:463509" /clone="InxoE:463509" /clone=lib="NHH_MGC_18" /tissue_type="large cell carcinoma" /tab.host="bp108 (phage-resistant)" /note="Organ: lung; Vector: poTB7; Site_1: Xho1; Site_2: EcoRI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor: Inboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and NIH_MGC Library. (Life Technologies). Note: this is a 253 a 195 c 199 g 272 t	Simil 3; C	TAATTAAAGGTCAAACGCAGAA 8 				AATGTGGCCTACTTTACGACCA			
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	70 =	0,2	Ouery Match Best Local Matches 728	829 GC 11 2 GC	888 CT 62 CT	948 TT 122 TT	1008 AAJ 111 182 AAJ	1068 CTA	194	1128 AAA	1188 GAT 238 GAT
AC VE SC	RE	FE7	BASE	OMŽ	Qy Qa	QY	Oy Dp	Qy Dp	Qy	qq	Qy Db	Qy Dp

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Email: cgapbs-rémail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:

NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
IC Lobase; 1 to 483)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
1248 GITATICTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGT 1307
                                                                        1308 CCGCAAGCACACTCCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCT 1367
                                                                                                                                              1428 TGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATGTCGTCC 1487
                                                                                                                                                                                                                                                                                             1488 TITCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGC 1547
                                                                                                                                                                                                                                                                                                                                                                       1548 CCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGG 1607
                                                                                             297 -----GCACCCTTTGACAATGATAATGCT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                           1608 AGTCCCTGCGTATTATCTCTTTATTATGGGACAAGAAACCCAGGTGGTTTAGAATAAT 1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1668 GTCAGAGAAAATAACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAAGAAGATA 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW2U5572
483 bp mRNA linear EST 02-DEC-1
UI-H-BIL-adt-h-02-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2718171 3', mRNA sequence.
                                                                                                                                                                                                                                          1728 GTTATGAACTAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAA 1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2713171"
/clone_lib="NCI_CGAP_Sub3"
/lab_host="DH10B (Life Technologies)"
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www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                       297 -----
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AW205572/c
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EST 08-MAR-2002
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1 (bases 1 to 511)
Myntz,M. K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.
Expression Profile and Genome Location of CDNA Clones from an Infant Human Trabecular Meshwork Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWT023 Human Trabecular Meshwork cDNA library Homo sapiens CDNA 5'
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1366 CTCTTCTCTGGAGACCTCGACAGTCTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTT 1425
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                                                                                                                                                                         /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               946 TATTATGGAATGTATGCATATGCTGGCTTTTACCTCAACTTTGTTACTGAAGAAGTA 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 516
                                                                                                                                                                                                                                                                                                                                                                                                  61 TAAAACCCTGAAAAACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATT 120
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Pred. No. 4.4e-88;
0; Mismatches 2; Indels 0.
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                                                                                                /clone="DKFZp686C09156"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
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                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                110 g
                                                                                    /db_xref="taxon:9606
                                                                                                                                                     "adult"
                                                                                                                                                      /dev_stage="adult
/lab_host="DH10B"
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99.6%;
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BM887840
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BG490131 919 bp mRNA linear EST 27-MAR-2001 602519050F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4637509 5',
                                                                                                                                                                                                                                                                                     Anote—Vector: pcDNA3; Site_1: BCORI; Site_2: BCORI; Human chole—Ibrary made from mRNA isolated from trabecular meshwork cells established fom eyes from 6 individuals, and seeks to 2 years. Cells were harvested at passages 3 through 6. Invitrogen made a unidirectional cDNA library from the mRNA from the frozen cells using a pcDNA3 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2056 AGAACCTTCAAATTGAAGACTGAGATTTTTCTGTATATATGGGTTTTGTAAAGATGGTTT 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1876 ATATICGAACTAATITCTAAGAAATTTAGTTATAACTCTATGTAGTTATAGAAAGTGAAT 1935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1996 GGAGAAAAGACTAGACAATTACTATGTGGTCATTCTCTACAACATATGTTAGCACGGCAA 2055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1696 AIAATACTGGAAGTTGTACCAGAAGAAGATAAGTTATGAACTAATGGACTTGAGATCTTG 1755 | 1696 AIAATACTGGAAGTTGTACCAGAAGAAGATAAGTTATGAACTAATGGACTTGAGATCTTG 392 | 451 ATAATACTGGAAGTTGTACCAGAAGAAGATAAGTTATGAACTAATGGACTTGAGATCTTG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1636 TGGGACAAGAAACCCAGGTGGTTTAGAATATGTCAGAGAAAATAACCAGAACATTACAA 1695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                      /db_xref="taxon:9606"
/clone_lib="Human Trabecular Meshwork cDNA library"
/tissue_type="eye"
Contact: Wirz-NK,
Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-6887
Email: wirtzm@obsu.edu
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.7%; Score 508.4; DB 14; Length 511; Similarity 99.6%; Pred. No. 3.1e-87;
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0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                1 others
                                                                                                                                                                                                                                        /cell_type="trabecular meshwork"
/dev_stage="2 week to 2 year old infants"
/lab_host="TOPlOF'"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2116 TACACACTACAGATGTCTATACTGTGAAAAG 2146
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                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                              Location/Qualifiers
                                                                                                                              Seq primer: T7 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         161
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		AL702210 DKFZp686C	BM887840 TMT023 Hu	BG490131 602519050	AW205572 UI-H-BII-	BG284501 602425373 BG284503 602408645
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42 Yz 588 3107 2457 5046			AL63572 AL63572 B1181265 UNL-P-FN- BM556677 AGENCOURT BQ682351 AGENCOURT BQ678193 AGENCOURT BQ681717 AGENCOURT AL635943 AL635943 AL105370 ESCALO	ALSO 1848 ALSO 1894 BALSO 1894 BALSO 1894 BALSO 243 1 ALSO 243 1 BQ 678 BALSO 1894 BAGENCOURT BQ 693707 AGENCOURT BG 6931004 AGENCOURT BG 693115 AGENCOURT BG 693115 AGENCOURT ALSO 263 ALSO 60271845 BM 62577 ciha Bu 6963289 UI-M-EQO-
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				35 1812 36 180 37 180 38 179 40 179 41 177 43 172 44 172

ALIGNMENTS

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New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-', pathology-', and
                          Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
                                                                                            Example 1; SEQ ID 7959; 47pp; English.
                                                                               developmental-specific genes
02-MAY-2001; 2001US-287724P.
              (COMP-) COMPUGEN INC.
                                           WPI; 2002-257383/30.
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the messenger RNAs that populate a genome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises conservation in the stanscribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a piological sample, in expression profiling studies, in qualitatively or consequences. The libraries are useful for detecting mRNAs from a piological sample, and splice variants of human or animal consequences. The libraries may also be used as specialised minicationary biological or pathological state, and so allowing the certifon of tissue- and pathological state, and so allowing the condition; to detect developmental specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA condition; to detect developmental specific genes; and to detect RNA condition; to detect developmental specific genes; and to detect RNA condition; to detect developmental specific genes; and to detect RNA condition; to detect developmental specific genes; and to detect RNA condition; but as sequences from rats, humans and mice, which are used in the sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cet fitpulpy. The sequences.

Sequence 60 BP; 14 A; 18 C; 11 G; 17 T; 0 other;

0; Gaps 2.7%; Score 60; DB 24; Length 60; 100.0%; Pred. No. 4e-15; tive 0; Mismatches 0; Indels Best Local Similarity 100.0 Matches 60; Conservative Query Match

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Search completed: April 16, 2003, 11:21:56 Job time : 528 secs

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21-SEP-2000; 2000US-0234274.
25-SEP-2000; 2000US-0234997
25-SEP-2000; 2000US-0234998.
26-SEP-2000; 2000US-0235484.
27-SEP-2000; 2000US-0235834.
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2000US-0246532.
2000US-0246609.
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29-SEP-2000; 2000US-0236327.
29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236368.
29-SEP-2000; 2000US-0236369.
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01-DEC-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to cyplement the patients own production of (I). Additionally, (I) polyucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK64950 and AAM82169
                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 GAAAGCCIGTIGTGTCCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGA 241
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                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 23451; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
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4.5%; Score 100; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.3e-32;
Matches 100; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                 Rosen CA, Barash SC, Ruben SM;
                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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                     2000US-0251989.
2000US-0251990.
                                                         11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
     2000US-0251869
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08-DEC-2000;
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23451.
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06-NOV-2001 (first entry)
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28-JUN-2000;
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                                                                                                                                                                                                                                                   02-MAR-2000;
                                                                                                                                                      09-AUG-2001
    ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         527 TGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTGG 574
                                    636 TGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATTTTGG 683
                                                                                                                                                                                                    Human colon tumour antigen polynucleotide SEQ ID NO:1307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 575 BP; 151 A; 122 C; 153 G; 141 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. ///
Best Local Similarity 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 1307; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK68639 standard; DNA; 123 BP.
                                                                                                                         ABL37718 standard; cDNA; 575 BP
                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-2000; 2000US-210899P.
20-FEB-2001; 2001US-270216P.
                                                                                                                                                                                                                                                                                                                                                            08-JUN-2001; 2001WO-US18557.
                                                                                                                                                                               08-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jiang Y, Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-114514/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                       WO200196388-A2.
                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                   20-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK68639;
                                                                                                                                                      ABL37718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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                                                                                                   RESULT 13
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AAZ16609 standard; cDNA; 800 BP.

12-OCT-1999 (first entry)

AAZ16609;

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The invention relates to an isolated polynuclectide (I) encoding a polypeptide (II) comprising at least a portion of a colon tumour the presence of a cancer in a patient. (I), (II) or antigen presenting cells expressing (I) is useful for stimulating and/or expanding T cells expressing (I) is useful for stimulating and/or expanding T cells presenting cells that express (I), under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

CC (I), (II), or antigen presenting cells that express (II) are useful for treating colon cancer in a patient by incubating CD4+ and/or CD8+ T cells captaing colon cancer in a patient by incubating CD4+ and/or CD8+ T cells captain an effective amount of the proliferate of administering to the patient an effective amount of the proliferated T cells, thus inhibiting carcines and pharmaceutical compositions for prevention and treatment corrects. (I), (II) or (III) is useful for detection, diagnosis and/or cancers. (I), (II) or (III) is useful for detection, diagnosis and/or therapy of human colon cancer. (I) is useful as a probe or primer for concers. (I), (II) or inhibiting expression of (III) in tumour cells.

CC follon malignancies and for the diagnosis and monitoring of such therapy of human colon cancer. (I) is useful as a probe or primer for cancers. (I), (II) or III) is useful as a probe or primer for concers coding malignaries of the invantion of (III) in tumour cells.
                                                                                                                                                                                                                                                                                           Novel isolated polynucleotide encoding a polypeptide comprising a portion of colon tumour protein, useful for detection, diagnosis and therapy of human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 ACCATCATTGGAGCAGGAATCTTCATCTCCTAAGGGCGTGCTCCAGAACACGGGCAGC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 GTGGGCATGTCTGACCATCTGGACGGTGTGTGGGGGTCCTGTCACTATTTGGAGCTTTG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 GTGGGCATCTCTGACCATCTGGACGGTGTGGGGGTCCTGTCACTATTGGAGCTTTG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 269; DB 24; Length 59; Pred. No. 1.5e-102;
                                                                                                                                                                                                                      Clapper JD, Wang A, Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 596 BP; 160 A; 151 C; 126 G; 158 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100.0%; Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 174; 220pp; English.
                                                                                             09-JUN-2000; 2000US-210821P.
                                                          08-JUN-2001; 2001WO-US18577.
                                                                                                                    18-DEC-2000; 2000US-256571P.
10-MAY-2001; 2001US-290240P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 269; Conservative
                                                                                                                                                                                                                Jiang Y, Hepler WT,
                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                        WPI; 2002-139708/18.
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Suspected of being cancerous, where product is anocaded by one of the 5248 polynucleotides can be used as a source of primers and probes, which can polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, detection of polymorphisms. Polypeptides encoded by the polynucleotides and can be used for raising antibodies for experimental, diagnostic and can be used for raising antibodies for experimental, diagnostic and arrays for diagnostics (which may be used to determine function of an two cells (e.g. to identify abnormal or diseased tissue in a human, to cancer). The polynucleotides in expression levels between diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a library of human polynucleotides comprising the sequences given in AA112532 to AA21779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell
                                                                                                                                                        detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 TGACCATCTGGACGGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAAT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                         Human; gene; gene expression product; diagnosis; therapy; probe;
                                                                                                        Human gene expression product cDNA sequence SEQ ID NO:4079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Bscobedo J, Garcia PD, Garcia V, Glese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 800 BP; 199 A; 166 C; 202 G; 211 T; 22 other;
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100.0%; Pred. No. 2.9e-35;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1934; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                      98US-0072910.
98US-0075954.
                                                                                                                                                                                                                                                                                                                   99WO-US01619.
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Escobedo J, Galt.,
Jones WL, Kassam A, Kenne
Jones WL, Leshkowitz D, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-494092/41.
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                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                             WO9938972-A2.
                                                                                                                                                                                                                                                                                                                 28-JAN-1999;
                                                                                                                                                                                                                                                                              05-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                  03-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1998;
03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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514 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 573

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RESULT 12 AA216609

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WO200196390-A2
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                                                                                                                                                                genes correlated with a cancerous state of a mammalian cell, comprising genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test cancerous state of the differentially expressed gene product is correlated with a concerous state of the cell from which the test sample was derived. The polyuucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polyuucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and cerecting and mapping related genes. They can be used in diagnosis and corremensation on materatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, costrogen receptor-positive breast cancer, negative breast cancer, lung cancer, and colon cancer.
                                                                                                                                         libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; lung tumour protein; immunostimulant; cytostatic; gene therapy; antisense-therapy; vaccine; immune response; lung cancer; 20E10; ss.
                                             Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          778 GICAGCIGGAGCGCCCGGAICCAGAITITCTIAACCIITIGCAAGCICACAGCAAIICIG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   718 GCGATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                        AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 284; DB 21; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           898 GCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGC 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 GCCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.7%; Score 284; DB 41, Best Local Similarity 100.0%; Pred. No. 8.6e-109; Assmatches 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 300 BP; 80 A; 65 C; 66 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lung tumour-specific 20E10 5' cDNA.
                                                                                               Claim 1; Page 392; 1097pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD23462 standard; cDNA; 337 BP
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                    WPI; 2000-126369/11.
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The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and expanding release useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition useful for stimulating an immune responses, and for treating cancer. The lung tumour specific oligonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence is a cDNA encoding human lung tumour-specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CATAGAITITATCATATICIGGAITITITGGAITCITITGTITICICATCACTGGAITCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAAGCCIGITGTGTCCACCATCTCCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s MJ, Mohamath R, Secrist H, Benson DR, Indirias CY; Fling SP, Algate PA, Elliot M, Mannion J, Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAC 60
                                                                                                                                                                                                                                                                                                                                                                            New human lung-specific polynucleotides and polypeptides for the diagnosis and treatment of disease e.g. lung cancer –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; colon cancer; T cell expansion; tumour; EST; gene; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.6%; Score 281; DB 23; Length 337; 100.0%; Pred. No. 1.5e-107; ative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colon cancer expressed sequence tag, Seq ID no 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AGGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 337 BP; 103 A; 60 C; 93 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 334; 378pp; English.
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29-MAR-2000; 2000US-0538037.
05-JUN-2000; 2000US-0588937.
18-MG-2000; 2000US-0640878.
22-SEP-2000; 2000US-034517P.
01-NOV-2000; 2000US-0704512.
14-DEC-2000; 2000US-0738973.
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Matches 281; Conservative
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                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639201/73.
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The present invention describes a library of human polynucleotides comprising the sequences given in AA21253 to AA21779. Also described is a method of detecting differentially expressed genes correlated with the dancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell of the 5248 polynucleotide sequences given in AA212532 to AA21779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and
                                                              959 AIGCAIAIGCIGGCIGGITITACCICAACITIGITACTGAAGAAGTAGAAAAACCCIGAAA 1018
                                                                                                                           1019 AAACCATTCCCCTTGCAATATGTATCCATGGCCATTGTCACCATTGGCTATGTGCTGA 1078
                                                                                                                                                                                          1079 CAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGTGCAAATGCAGTGG 1138
                                                                                 899 CCTTTTCAGGAAGAATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGT 958
                                61 CCTTTTCAGGAAGAGTTTCAAGTATTACGCGGTTGCCACTGGCTTTTTATTATGGAATGT 120
                                                                                                                                                                                                             Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                     Human gene expression product cDNA sequence SEQ ID NO:1773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac R, Drmanac S;
arcia V, Giese K, Innis MA;
edy GC, Kita D, Labat I;
Pot D, Randazzo F, Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escobedo J, Garcia PD, Garcia V, Giese K, Inn
Jones WL, Kassam A, Kennedy GC, Kita D, Labat
Lamson G, Leshkowitz D, Pot D, Randazzo F, Re
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1061; 2479pp; English.
                                                                                                                                                                                                                                                                                                        AAZ14304 standard; cDNA; 288 BP.
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98US-0072910.
98US-0075954.
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98US-0080515.
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                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crkvenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-1998
                                                                                                                                                                                                                                                                                                                                        AAZ14304;
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therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
D, Kita D, Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                           959 ATGCATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAA 1018
                                                                                                                                                                                                                                                                                                                                                                                                                    1019 AAACCATTCCCCTTGCAATATGTATCCATGGCCATTGTCACCATTGGCTATGTGCTGA 1078
                                                                                                                                                                                                                                        839 TAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACG 898
                                                                                                                                                                                                                                                                                                 899 CCTTTTCAGGAAGAATTCAAGTATTACGCGGTTGCCACTGGCTTTTTATATATGGAATGT 958
                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                        Human colon cancer cell line polynucleotide sequence SEQ ID NO:871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; colon cancer; tumour; diagnosis; gene expression product;
                                                                                                                                                                                        Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1079 CAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGTT 1126
                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.9%; Score 288; DB 20; I 100.0%; Pred. No. 1.8e-110;
                                                                                                                                                  Sequence 288 BP; 81 A; 58 C; 59 G; 90 T; 0 other;
                                                                                                                                                                                         100.0%; Preu. ...
                                                                                                                    peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA00880 standard; cDNA; 300 BP.
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98US-0085537.
98US-0085696.
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98US-0105877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                           Matches 288; Conservative
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR ) CHIRON CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-0CT-1998
                                                                                                                                                                                 Query Match
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AA214962;

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The present invention describes a library of human polynucleotides comprising the sequences given in AA212532 to AA21779 Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell cancerous, where the gene product is encoded by one consequence and product is encoded by one coll the 5248 polynucleotide sequences given in AA212532 to AA217799. The polynucleotides can be used as a source of primers and probes, which can be used for availety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polynucleotides encoded by the polynucleotides for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct therapeutic purposes. The polynucleotides may also be used to construct therapeutic purposes. The polynucleotides may also be used to construct carrays for diagnostics (which may be used to determine function of an enrays for identify abnormal or diseased tissue in a human, to two cells (e.g. to identify abnormal or diseased tissue in a human, to two cells (e.g. to identify abnormal or diseased tissue in a human, to dence or the polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, or and the detection as a polynucleotides can also be used to correct for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1247 GGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATG 1306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1067 GCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGTTT 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1127 CAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CAPATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CGATCTTTGTTGCCCTCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTTTTGCTGTCTCCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.4%; Score 300; DB 20; Length 300; 100.0%; Pred. No. 1.8e-115; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                          Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 300 BP; 58 A; 76 C; 67 G; 99 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1211; 2479pp; English.
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98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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                                                                                                                                                                                                     (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
    28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
                                                                                                                              03-APR-1998;
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AAZ14962 standard; cDNA; 300 BP.

RESULT 7 AAZ14962

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The present invention describes a library of human polynucleotides comprising the sequences given in AZ12532 to AZ1779. Also described is comprising the sequences given in AZ12532 to AZ1779. Also described is cancerous state of a mammalian cell, comprising detecting at least one differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell differentially expressed gene product in a test sample from a cell of suspected of being cancerous, where the gene product is encoded by one polynucleotides can be used as a source of primers and probes, which can be used for avariety of purpose, e.g. detection of expression levels, be used for a variety of purpose, e.g. detection of expression levels, detection of polynucleotides and detection of polynucleotides and detection of polynucleotides can be used to construct therapeutic purposes. The polynucleotides may also be used to construct therapeutic purposes. The polynucleotides may also be used to construct characterially and to detect differences in expression levels between a arrays for diagnostics (which may be used to determine function of an arrays for add to detect differences in a expression levels between the polynucleotides and determine function of an arrays for add to detect differences in a expression levels between the polynucleotides and an arrays for diagnostics (which may be used to determine function of an arrays for add to detect differences in a expression levels between the polynucleotides and an arrays for diagnostics which may be used to determine function of an arrays for add to detect differences in a expression levels between the polynucleotides and an arrays for diagnostic and an arrays of the polynucleotides and arrays for diagnostic and to detect differences in the expression levels between the polynucleotides and arrays for diagnostics (which may be used to determine the polynucleotides and arrays for diagnostics and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
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                                                                                                                                                   Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profilling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 300;
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                                                                                                      Human gene expression product cDNA sequence SEQ ID NO:2431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glese K, Innis MA;
Kita D, Labat I;
andazzo F, Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human genes and their expression products which are differentially expressed in different cell types
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Pred. No. 1.8e-115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escobedo J, Garcia PD, Garcia V, Giese K, Inn
Dones WL, Rassam A, Kennedy GC, Kita D, Labat
Lamson G, Leshkowitz D, Pot D, Randazzo F, Re
Stache-Crain B, Sudduth-Klinger J, Williams LT;
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Matches 300; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1207; 2479pp; English.
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98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                          WO9938972-A2.
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24-FEB-1998;
31-MAR-1998;
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                                                                   12-0CT-1999
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The
1834 ATAAACAAAAGGGGTCAGTTATTTTTATTCATATATTTTAGCATATTCGAACTAATTTCT 1893
                   1894 AAGAAATITAGTTATAACTCTATGTAGTATAGAAAGTGAATATGCAGTTATTCTATGAG 1953
                                                                            1954 TCGCACAATTCTTGAGTCTCTGATACCTACCTATTGGGGTTAGGAGAAAAGACTAGACAA 2013
                                                                                                                                                  1788 TCGCACAATTCTTGAGTCTCTGATACCTACTATTGGGGTTAGGAGAAAAGACTAGACAA 1847
                                                                                                                                                                                 2014 TTACTATGTGGTCATTCTCTACAACATATGTTAGCACGGCAAAGAACCTTCAAATTGAAG 2073
                                                                                                                                                                                                  Human, gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene expression product cDNA sequence SEQ ID NO:3998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human genes and their expression products which are differentially expressed in different cell types
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Garcia PD, Garcia V, Giese K, Innis MA;
Kassam A, Kennedy GC, Kita D, Labat I;
Leshkowitz D, Pot D, Randazzo F, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                            2074 ACTGAGATTTTTCTGTATATATGGGTTTTG 2103
                                                                                                                                                                                                                                                             1908 ACTGAGATTTTTCTGTATATGGGTTTTG 1937
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                                                                                                                                                                                                                                                                                                                                                  AA216528 standard; cDNA; 772 BP.
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98US-0075954.
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98US-0080515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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24-FEB-1998;
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polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                        1099 ACCATTAATGCTGAGGAGCTGCTTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCG 1158
                                                                                                                                                                                                                                                                                                                                                                                                                          1159 CTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCC 1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1279 CITCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATT 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1459 CGATACAAATGCCCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCA 1512
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                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                      Sequence 772 BP; 175 A; 183 C; 158 G; 248 T; 8 other;
                                                                                                                                                                                                                                                                                          18.5%; Score 414; DB 20; I 100.0%; Pred. No. 3.7e-163; tive 0; Mismatches 0;
                                                                                                                                                                                                                          peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ14980 standard; cDNA; 300 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                             proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomator. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forenaics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTCAATGTGAAATGCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 753
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                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
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                                                                                                                                                                                                                                                                            Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.8%; Score 1719; DB 22; Length 1958;
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0; Mismatches
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                                                                                                                                                                                                                                                                                               Zhang J,
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
                                                                                                                                                          25-JAN-2001; 2001WO-US02687
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                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                       WO200154477-A2.
                                                                                Homo sapiens
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                   528 ATTCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGGCATAACTGTA 587
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bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuropithelial cells autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
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                                                                                                                                                                                                                                    334 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTGGC 393
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                                                                                                                                               Sequence 1958 BP; 499 A; 418 C; 424 G; 617 T; 0 other;
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0; Mismatches
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99.9%;
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1008 TCATTAGCAGIICCGAICTITGIIGCCCICCICCIGCIIIGGCICCAIGAACGGIGGIGG 1067
                                     1234 ITTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
                                                    1294 TCCATGATTCATGTCCGCAAGCACACTCCTACCAGCTGTTATTGTTTTGCACCCTTTG 1353
                                                                                                                                           ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCTCAGTTTTGCC 1413
                                                                                                       1414 AGGIGGCTTTTTATTGGGCTGGCAGTTGCTGGCTGATTTATCTTCGATACAAATGCCCA 1473
                                                                                                                                                                                                                    1248 AGGIGGUTITITATIGGGCIGGCAGTIGCTGGCTGATTTATCTICGATACAAAIGCCCA 1307
                                                                                                                                                                                                                                             1474 GATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGC 1533
                                                                                                                                                                                                                                                            CICITCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1593
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2134 ATACTGTGAAAAGTGTTTTCAATTCTGAAAAAAAGCATACATCATGATTATGGCAAAGAG 2193
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1414 AGGIGGCITITITAITGGGCIGGCAGTIGCIGGGCIGAITITAICITCGATACAAATGCCCA 1473
                                                                                                                                                                GATATGCATCGTCCTTTCAAGGTGCCACTGTTCATCCCAGCTTTGTTTTCCTTCACATGC 1533
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                                                                                                                  1294 ICCATGATTCATGTCCGCAAGCACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTG 1353
                                                               1238 TCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATGTTTTGCACCCTTTG 1297
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ABA09201 standard; cDNA; 1958 BP.

ABA09201 ID ABA RESULT 3

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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of detecting the nucleotides of nucleotides of the invention. Although novel, many of the bind to polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence of potential therapeutic applications. The polypeptides of the invention may have various activities; is tem cell growth factor activity; have various activities; stem cell growth factor activities; haematopoisals regulatory activity; tissue growth activity; immunomodulatory activity; activin. or inhibin-related activities; chemotactic or chemokinetic activities; haemactatic, thromboth or may be conditions activities; activities; polypeptides and nucleotides of thrombolytic cativities; cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid call cancers, haematopoietic disorders (e.g., asthma or arthritis), arterial ischaemia, bone disorders (e.g., asthma or arthritis), arterial schaemia, bone disorders (e.g., sobperorsis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and vascular growth. Polypeptides involved with tissue regeneration and vascular growth. Polypeptides involved with tissue regeneration and bealing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral,
                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                     bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinfinamatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                               Human cystine/Glu transporter homologue cDNA, SEQ ID NO:977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 835; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                               11-JAN-2002 (first entry)
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                 ABA09201;
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1801 TITCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAAGGAGTCAGTTATTTTA 1860
                        1861 TICATATATITTAGCATATICGAACTAATTICTAAGAAATTTAGTTATAACTCTATGTAG 1920
                                     1921 TTATAGAAAGTGAATATGCAGTTATTCTATGAGTCGCACAATTCTTGAGTCTCTGATACC 1980
                                                                                    TACCTATTGGGGGTTAGGAGAAAAAGACTAGACTATTACTATGTGGTCATTCTCTACAACAT 2040
                                                                                                                                    2101 TIGTAAAGAIGGITITACACACTACAGAIGICTAIACIGIGAAAAGIGITITCAATICIG 2160
                                                                                                                                                                                                                                  2161 AAAAAAACCATACATCATGATTATGGCAAAGAGGAGAGAAGGTAGAGCTGTTCTTAAATT 2220
                                                                                                                                                                                                                                                                                   2161 AAAAAAAGCATACATGATGATTATGGCAAAGAGGAGGAGGAAGGTAGAGCTGTTCTTAAATT 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulant; cytostatic; gene therapy;
immune response; lung cancer; 14F10; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and
                                                                                                                                                                      2041 ATGTTAGCACGGCAAAGAACCTTCAAATTGAAGACTGAGATTTTTCTGTATATATGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human lung-specific polynucleotides and polypeptides for the diagnosis and treatment of disease e.g. lung cancer –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mannion J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lung tumour-specific 14F10 full length cDNA.
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Henderson RA, Fling SP, Algate PA, Elliot M,
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14-DEC-2000; 2000US-0738973.
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2000US-234517P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense-therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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their antigen-presenting cells are useful for stimulating and/or expanding I cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition useful for stimulating an immune response, and for treating cancer. The lung tumour specific oligonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence
                                                                                                                                                                                                 334 GAGAAAGIGCAGCIGAAGAGGAAAGICACTITACIGAGGGGAGICICCATIAICATIĞGC 393
                                                                                                                                                                                                                394 ACCATCATTGGAGCAGGAATCTTCATCTCTTAAGGGCGTGCTCCAGAACACGGGCAGC 453
                                                                                                                                                                                                                                                                                             397
                                                                                                                                                                                                                                                                                                             GIGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGGTCCTGTCACTATTTGGAGCTTTG 513
                                                                                                                                                                                                                                                                                                                             573
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                                                                                                                                                                                 ;
0
                                                                                                                                                    Length 5981;
                                                                                                                 Sequence 5981 BP; 1858 A; 1029 C; 1098 G; 1996 T; 0 other;
                                                                                                                                                                                Indels
                                                                          diagnosis, detection and treatment of lung cancer. The is a CDNA encoding human lung tumour-specific protein.
                                                                                                                                                   DB 23;
                                                                                                                                                                              0;
                                                                                                                                                       100.0%; Pred. ...
                                                                                                                                                83.4%; Score 1867;
                                                                                                                                                                         Matches 1867; Conservative
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The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and their antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition useful for stimulating an immune responses, and for treating cancer. The lung tumour specific oligonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence is a cDNA encoding human lung tumour-specific protein.
New human lung-specific polynucleotides and polypeptides for the diagnosis and treatment of disease e.g. lung cancer ^{-}\,
                                                                                                                                                                                     Claim 1; Page 332; 378pp; English
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Sequence 2239 BP; 619 A; 444 C; 493 G; 683 T; 0 other;

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GCATTHGGACGCTACATTCTGGAACCATTTTTATTCAATGTGAAATCCCTGAACTTGCG 720 661 GCATTIGGACGATACATTCIGGAACCATTTTTATTCAATGIGAAATCCCIGAACTIGCG 720 721 ATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTC 780 601 GTACGAGICTGGGIGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTG 660 GIGIGIGGGGTCCTGTCACTATITGGAGCTTTGTCTTATGCTGAATTGGGAACAACTATA 540 541 AAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGTCCATTACCAGCTTTT 600 TCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACG 480 GIGIGIGGGGICCIGICACIAITIGGAGCIIIGICTIAIGCIGAATIGGGAACAACTAIA 540 240 361 ACTITACTGAGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATC 420 GCCTTTTCAGGAAGAGGCCCTTTTCAGGAAGAGAAAAGTGCAGCTGAAGAGGAAAGTC 360 61 AGAATTAAGGAAAAAGAAAGAAAGAAAAAGAGAGAGGAAATTCCAGGCCAATTGTGG 120 CATAGATTTATCATATTCTGGATTTTTGGATTCTTTTGTTTTTCTCATCACTGGATTCA 180 121 CATAGATITTATCATATICTGGATTTTTTGGATTCTTTTGTTTTCTCATCACTGGATTCA 180 241 AGGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGAC 300 Gaps GTACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTG GGAAAGCCTGTTGTGTCCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGG DB 23; Length 2239; ; 0 0; Indels Best Local Similarity 100.0%; Pred. No. 0; Matches 2239; Conservative 0; Mismatches 100.0%; Score 2239; 100.0%; Pred. No. 0; Query Match 421 481 481 601 301 301 ρp 8 δ g δλ g 8 ò ŏ δ g g 8 ò g ò õ ŏ a õ g õ õ g

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PRIOR APPLICATION NUMBER: US 60/357,600 PRIOR FILING DATE: 2002-02-15 NUMBER OF SEQ ID NOS: 54 SOFTWARE: Patentin version 3.1
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1234 TITGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
                         1294 TCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTATTGTTTTGCACCCTTTG 1353
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CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR PELICATION NUMBER: US 60/338,733
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
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TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EXO2-080C
CURRENT APPLICATION NUMBER: US/10/163,866
FRIOR APPLICATION NUMBER: US 60/296,076
FRIOR APPLICATION NUMBER: US 60/296,076
FRIOR FILING DATE: 2001-06-05
FRIOR FILING DATE: 2001-10-10
FRIOR FILING DATE: 2001-10-10
FRIOR FILING DATE: 2001-10-22
FRIOR FILING DATE: 2001-10-22
FRIOR FILING DATE: 2001-0-22
FRIOR FILING DATE: 2001-0-22
FRIOR FILING DATE: 2001-0-22
FRIOR FILING DATE: 2002-02-15
FRIOR FILING DATE: 2002-02-15
FRIOR FILING DATE: 2002-02-15
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1328 GIGITICTGGIGATAGIGCCCCTCTICACTGACACCATTAAITCCCTCATIGGCATCGGG 1387
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                                1594 ATCACTCTGACTGGAGTCCCTGCGTATT 1621
                                                   1388 ATTGCCCTTTCTGGAGTCCCTTTCTACT 1415
                                                                                                                                                    ; Sequence 8, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
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Matches 720; Conservative
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
                                                                                                                                                         963 TCTTTGCCTCTACTCTGCCCTCTTCTTACTCAGGTTGGGACACCCTTAATTTTGTA 1022
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843 TACGCCAAGGTCGTAGCGCTCATTGCCATTGTCATGGGCCTTGTTAAACTGTGCCAG 902
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Publication No. US20030027188A1
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APPLICANT: EXELIXIS, INC.

TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-080C

CURRENT APPLICATION NUMBER: US/10/163,866

CURRENT FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: US 60/296,076

PRIOR APPLICATION NUMBER: US 60/328,605

PRIOR PELLING DATE: 2001-10-10

PRIOR PELLING DATE: 2001-10-2

PRIOR PELLING DATE: 2001-10-2

PRIOR PELLING DATE: 2001-10-2

PRIOR PELLING DATE: 2001-10-2

PRIOR PELLING DATE: 2002-02-15

PRIOR APPLICATION NUMBER: US 60/357,600

PRIOR APPLICATION NUMBER: US 60/357,600

PRIOR PELLING DATE: 2002-02-15

PRIOR PELLING DATE: 2002-02-15
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             ----GAGAAAGTGCAGCTGAAGGTCA 133
                                             362 CITTACTGAGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGGAATCTTCATCT 421
                                                           16.9%; Score 379.2; DB 9; Length 1581; 55.9%; Pred. No. 1.6e-91;
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; Publication No. US20030027188A1
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                                                                                                                                                                                                                                                                                                                                                                         694 AITCAATGTGAAATCCCTGAACTTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 753
                                                                                                                                                                                                                                                                                                                                                                                                    488 CCCAGCTGTGATCCCCCCATACCTGGCCTGCTGCTGCTTGCATATGTCTG 547
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                                                                                                                                                                                                                                                                                                                       248 TATEGGATETCACTGATTGTGTGGGCCCATTGGTGGGGCTCTTCTCTGTTGTGGGTGCCCTT 307
                                                                         514 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 573
                                                                                                    574 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGC 633
                                                                                                                                                                                                                     368 GAGGCCTTTGGGGGCCTTCATGCCTTCATCCGCCTGTGGGTCTCACTGCTAGTTGTTGAG 427
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	Oy 1202 TCTCCTGCTTTGGCT Db 995	QY 1262 CGTCTCGAGAGGGTC Db 995	Oy 1322 CTCTACCAGCTGTTA	Qy 1382 TCGACACTCTTTGA (111111111111111111111111111111111111	1442	OY 1502 TGTTCATCCCAGCTTT	OY 1562 CGGACCCATTAGTAC 	RESULT 12 US-10-163-866-32	Sequence 32, Application Sequence 32, Application Publication No. US20300 GENERAL INFORMATION: APPLICANT: EXELIXIS, IN	TILE REFERENCE: EXO2-08 CURRENT APPLICATION UNIV	FRICK APPLICATION NUMBER PRICK APPLICATION NUMBER PRICK APPLICATION NUMBER PRICK FILING DATE: 2001	; PRIOR APPLICATION NUMBE ; PRIOR FILING DATE: 2001 ; PRIOR FILING DATE: 2002	PRIOR APPLICATION NUMBER PILING DATE: 2002 NUMBER OF SEQ ID NOS: 5 SOFTWARE: Patentin vers	; SEQ 1D NO 32 ; SEQ 1D NO 32 ; TYPE: DNA ; ORGANISM: HOMO sapiens	Query Match Best Local Si Matches 513:	OY 182 GAAAGCCTGTTGTGTCTCTCTCTCTCTCTCTCTCTCTCTC	242	
	Gans 2.	-	301 127	361	155 421	215 481 275	3 54 1 3 3 5	601 305	661 455	721 515	781 525	841 635	901 695		1021 815	1081 875	E.	ū
; TYPE: DNA STATE HOMO Sapiens US-10-163-866-53	46.8%; Score 1047.4; DB 9; Length 1268; Pred. No. 1.7e-271; Pred. No. 1.7e-271; 3; Conservative 0; Mismatches 1; Indels 170;	GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGG 			CTTTACTGAGGGGAGTCTCCATTATCATTGGCACCATCATTGGAGCAGCAACACTCATCT [CTCCTAAGGGCGTGCTCCAGAACACGGCAGGCAGGGCATGTCTCTGCAGCGACGGCGTGCTCTGAACACGGCAGGCA	TGTGTGGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACACTATA	AGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGTCCATTACCAGTTTTG 	TACGAGTCTGGGTGGAACTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGG			782 GCTGGAGCGCCCGGATCCAGATTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATA 8 				CCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGTGAGAA 108	ATGIGGCCIACTITACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAG 1141 	TGACCITITCTGAGGGGCTACTGGGAAATTTCTCATTAGCAGTFCCGATCTTTGTTGCCC 1201
TYPE ORGA S-10-16	Query Match Best Local Matches 123	y 182 b 30	Y 242	302 302	362	422	482	336	396	662 456	722	782 576	842	902		1022 (1082 8	1142
D		QY Db	QV Db	Oy Db	QQ Qp	Qy Db	Qy Db	QQ Dp	Oy Db	Qy Db	Qy Db	Oy do	Oy Db	Qy Db	Oy Dp	λ _, d	Ογ Db	ΟŊ

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775 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
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                                   ICCATGAACGGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTG 1261
                                                                                ACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTC 1321
                                                                                                                                              TIGITITGCACCCTITGACAATGATAATGCTCTTCTCTGGAGACC 1381
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R: US 60/328,605
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SR: US 60/357,600
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                                                                                                               61.3%; Score 1373.4; DB 9; Length 2000; 96.0%; Pred. No. 0; Live 0; Mismatches 6; Indels 54;
                                                                                                                                                                                             PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
PRIOR PELLING DATE: 2002-015
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
                                                                                                                                    Matches 1441; Conservative
                                                                                          ORGANISM: Homo sapiens
                                                                                                                             Local Similarity
                                                                        2000
                                                                                                  US-10-163-866-34
                                                                 SEQ ID NO 34
                                                                                  TYPE: DNA
                                                                                                                    Query Match
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Sequence 53, Application US/10163866

Publication No. US20030027188A1

GENERAL INFORMATION:

APPLICANT: EXELIXIS, INC.

TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

TITLE OF INVENTION: SLC7s AS WODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

FILE REFERENCE: EX02-080C

CURRENT FILING DATE: 2002-06-05

PRIOR PELING DATE: 2001-06-05

PRIOR PELING DATE: 2001-10-05

PRIOR PELING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/338,733

PRIOR APPLICATION NUMBER: US 60/338,733

PRIOR PELING DATE: 2001-10-22

PRIOR PELING DATE: 2001-10-22

PRIOR PELING DATE: 2002-02-15

PRIOR PELING DATE: 2002-02-15

PRIOR APPLICATION NUMBER: US 60/357,600

PRIOR PELING DATE: 2002-02-15

PRIOR PELING DATE: 2002-02-15

PRIOR APPLICATION NUMBER: US 60/357,600

PRIOR PELING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 54

SEQ ID NOS: 54

SEQ ID NO 53:

**CONTACT OF THE P53 PATHWAY AND METHOR APPLICATION SET OF THE P53 PATHWAY APPLICATION SET OF THE P53 PATH APPLICATION SET OF THE THE P53 PATH APPLICATION SET OF THE THE THE P53 PATH APPLICATION SET O
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1022 CCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAA 1081
                                  1082 ATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAG
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TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                        Query Match
63.9%; Score 1431.8;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1497; Conservative 0; Mismatches
                                                          PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
SOFTWARE: PALENTH: 1528
SEO ID NO 52
LENGTH: 1528
FRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 52
              FILE REFERENCE: EX02-080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: EXELIXIS;
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-080C
CURRENT APPLICATION WOMBER: US/10/163,866
CURRENT PILING DATE: 2002-06-05
PRIOR APPLICATION WOMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-10-10
PRIOR PLICATION NUMBER: US 60/338,605
PRIOR FILING DATE: US 60/338,733
                                                            962 CATAIGCIGGCITGTITACCICAACITIGITACIGAAGAAGIAGAAAAACCCIGAAAAA 1021
                                                                                                                      1022 CCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAA 1081
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902 TITCAGGAAGAGITCAAGIAITACGCGGTIGCCACIGGCIITTIAITAIGGAAIGIAFG 961
                   1262 CGTCTCGAGAGGGTCACCTTCCAGAATCCTCTCCATGATTCATGTCCGCAAGCACACTC 1321
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; Publication No. US20030027188A1
; GENERAL INFORMATION:
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; Sequence 52, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
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                                   APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC75 AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE TITLE PEPERBUCE: EX02-080C CURRENT APPLICATION NUMBER: US/10/163,866 CURRENT FILING DATE: 2002-06-05
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                                                                                       CURRENT FILING DATE: 2002-06-05
PRIOR PILING DATE: 2002-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2011-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR PILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
    sequence 33, Application US/10163866; Publication No. US20030027188A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                       SOFTWARE: Patentin version 3.1
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Best Local Similarity 96.59
Matches 1519; Conservative
                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens US-10-163-866-33
                                                                                                                                                                                                                                                                      SEQ ID NO 33
LENGTH: 1542
US-10-163-866-33
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                                                                                         962 CATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAA 1021
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                                        GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REPERENCE: EXO2-080C
CURRENT APPLICATION NUMBER: US/10/163,866
CURRENT FILING DATE: 2002-06-05
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                                                                                                                             PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR PELICATION NUMBER: US 60/328,605
PRIOR PELICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR PLICATION NUMBER: US 60/338,733
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR PRIOR FILING DATE: 2002-02-15
                Sequence 30, Application US/10163866
Publication No. US20030027188A1
                                                                                                                                                                                                                                                                                                                                                                                          Match
Local Similarity 96.6%; Pre
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                Matches 1606; Conservative
                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
-10-163-866-30
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                                                                                                        182 GAAAGCCTGTTGTCTCCACCATCTCCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGA 241
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                                                        Length 2482;
                                                                                 3; Indels
                                                           DB 9;
                                                        84.3%; Score 1888.2;
97.1%; Pred. No. 0;
Live 0; Mismatches
                                                                                Best Local Similarity 97.1
Matches 1965; Conservative
                         ORGANISM: Homo sapiens
                                                                          Similarity
LENGTH: 2482
                                      US-10-163-866-29
              TYPE: DNA
                                                                Query Match
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2102 TGTAAAGATGGTTTTACACACTACAGATGTCTATACTGTGAAAAGTGTTTTCAATTCTGA 2161
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                                                                         1262 CGTCTCGAGAGGGTCACCTTCCAGAATCCTCTCCATGATTCATGTCCGCAAGCACACTC 1321
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1142 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCC 1201
               1145 TGACCTTTTCTGACCGCTACTGGAAATTCTCATTAGCAGTTCCGATCTTTGTTGCCC 1204
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SPECIANT: EXELIXIS, INC.

TITLE OF INVENTION: SLC78 AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILLE REFERENCE: EX02-080

CURRENT APPLICATION NUMBER: US/10/163,866

CURRENT FILING DATE: 2002-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-25

PRIOR PLING DATE: 2002-15

PRIOR PRIOR APPLICATION NUMBER: US 60/357,253

PRIOR PLING DATE: 2002-02-15

PRIOR PRILING DATE: 2002-02-15

PRIOR PRILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PATENTIN VERSION 3.1
                1502 TGTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGGTTGCCCTTTCCCTCTATT 1561
                                                         1562 CGGACCCATITAGTACAGGGAITGGCTTCGTCATCACICTGACTGGAGTCCCTGCGTATT 1621
                                                                        1622 ATCTCTTTATTATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATA 1681
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; Publication No. US20030027188A1
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qq		CCTAAATAGCATGAGTGTCAG 72	
yo 4	723 CTGGAGCGCCCGGATCCAGATT	ticttaaccittigcaagcicacagcaaticigataat 842 	
}	843 TATAGTCCTGGAGTTATGCAG	£ = £	
k o d	903 TTCAGGAAGAGATTCAACTAT 	¥ – ¥	
1 & E	963 ATATGCTGGCTGGTTTTACCT 967 ATATGCTGGCTGGTTTTACCT	CAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAAAC 1022 	
y d	1023 CATTCCCCTTGCAATATGTAT 1013 CATTCCCTTGCAATATGTAT 967 CATTCCCTTGCAATATGTAT		
ر م	1083 TGTGGCCTACTTTACGACCAT	TAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGT 1142 	
8 6 1	1143 GACCITITCIGAGCGGCTACT	GGGAAATTCTCATTAGCAGTTCCGATCTTGTTGCCCT 1202 	
on ko	1203 CTCCTGCTTTGGCTCCATGAA	SGTGGTGTTTGCTGTCTCCAGGTTATTCTATGTTGC 1	
g V	1147 CTCCTGCTTTGGCTCCATGAA	SGRGGIGITIGGIGICICAGGIIANICATICAGGIIANICATICAGGIIANICATICAGGIIANICATICAGGIIANICAGGII	
qq	1207 GTCTCGAGAGGGTCACCTTCC	AGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCC 126	
oy Dp	Oy 1323 TCTACCAGCTGTTATTGTTTTGG 	PACCCTTTGACAATGATAATGCTCTTCTCTGGAGACCT 138 	
ογ	1383 CGACAGTCTTTTGAATTTCCT	CAGTTTTGCCAGGTGGCTTTTTATTGGGCTGCCAGTTGC 1442 	
g ö	1443 TGGGCTGATTTATCTTCGATA	CAAATGCCCAGATATGCATCGTCCTTTCAA	
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Š Š	1503 GTTCATCCCAGCTTTGTTTTC	COTTCACAIGCOTCTTCAIGGTIGCCCTTTCCCTCTATTC 1562 	
Z Z	1563 GGACCCATTTAGTACAGGGAT	TGGCTTCGTCATCACTTGACTGGAGTCCTGCGTATTA 162:	
QQ	1507 GGACCCATTTAGTACAGGGAT	regettesteateactesactesagrecetsestata 156	
Qy Db	1623 TCTCTTTATTATATGC	sgacaagaaacccaggtgtttagaataatgtcagagaaataac 1682 	
٥y	1683 CAGAACATTACAAATA	TGTACCAGAAGATAAGTTATGAACTAATGG 174	
QQ	1627 CAGAACATTACAAATAAT	ggaagttgtaccagaagaagataagttatgaactaatgg 168	
Qy	1743 ACTTGAGATCTTGGCAATCT	GCCCAAGGGGAGACACAAAATAGGGATTTTTACTTCATTT 1802	
a D	1687 ACTTGAGAICTIGGCAAICI	SCCCENGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
Qy	1803 TCTGAAGTCTAGAGAATTA		

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TITLE OF INVENTION: SACURA SA MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE TITLE OF INVENTION: SLC75 AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE FILE REFERENCE: EXO2-080C CURRENT APPLICATION NUMBER: US/10/163,866 CURRENT FILING DATE: 2002-06-05 PRIOR FILING DATE: 2001-06-05 PRIOR FILING DATE: 2001-10-10 PRIOR FILING DATE: 2001-10-10 PRIOR FILING DATE: 2001-10-10 PRIOR FILING DATE: 2001-10-12 PRIOR FILING DATE: 2001-10-12 PRIOR FILING DATE: 2001-0-15 PRIOR FILING DATE: 2002-02-15 PRIOR FILING DATE: 2002-02-15
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                                       1863 CATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATGTTGTT 1922
1807 CATATATTTAGCATATTCGAACTAATTTCTAAGAATTTAGTTATAACTCTATGTAGTT 1866
                                                                                                                       1923 ATAGAAAGTGAATATGCAGTTATTCTATGAGTCGCACAATTCTTGAGTCTCTGATACCTA 1982
                                                                                                                                              1983 CCTATTGGGGTTAGGAGAAAAGACTAGACAATTACTATGTGGTCATTCTCTACAACATAT 2042
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84.9%; Score 1900.2; DB 9; Length 3144;

Best Local Similarity 97.2%; Pred. No. 0;

Matches 1966; Conservative 0; Mismatches 3; Indels 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 31, Application US/10163866; Publication No. US20030027188A1; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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1267 TCTACCAGCTGTTATTGTTTTGCACCCTTTGACAATGATAATGCTCTTCTCTGGAGACCT 1326
                                                                   1383 CGACAGICTITIGAAITICCICAGTITIGCCAGGIGGCTITITAITGGGCIGGCAGIIGC 1442
                                                                                1443 TGGGCTGATTTATCTTGGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCACT 1502
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APPLICANT: Reed, Steven G.
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Reed, Steven G. Henderson, Robert A. Lodes, Michael J. Fling, Steven P. Mohamath, Raodoh

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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63 AAITAAGGAAAAAAAAAAAAAAAAAAAAAGAGAAATTCCAGGCCAATTGTGGCA 122
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                                                                  APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REPERPROCE: 210121,475C9
CURRENT APPLICATION NUMBER: US/09/738,973
NUMBER OF SEQ ID NOS: 587
                                                                                                                                                                                        FastSEQ for Windows Version 3.0
Algate, Paul A.
Secrist, Heather
Indirias, Carol Yoseph
                                            Benson, Darin R.
Elliot, Mark
                                                                                                                                                                                                                                                                                                      Best Local Similarity 97.5
Matches 2146; Conservative
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                                                                                                                                                                                                                    LENGTH: 5981
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1861 TTCATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATGTAG 1920
                                                              1861 TICATATITIAGCATATICGAACTAATTICTAAGAAATTIAGITATAACTCTATGTAG 1920
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: 02/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FatlsEQ for Windows Version 3.0
SEQ ID NO 48-1
LENGTH: 5981
                                                      Sequence 441, Application US/09854133 publication No. US20020183499A1 GENERAL INFORMATION:
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APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
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ORGANISM: Homo sapiens
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US-09-854-133-441
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THE THERAPY AND DIAGNOSIS OF LUNG CANCER
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                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 210.21.475c9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: S87
SOFTWARE: FastSEQ for Windows Version 3 0
                        APPLICANT: Mohamath, Readch, APPLICANT: Adgate, Paul A. APPLICANT: Secrist, Heather APPLICANT: Secrist, Heather APPLICANT: Benson, Darin R. APPLICANT: Eliot, Mark APPLICANT: Eliot, Mark APPLICANT: Mannion, Jane APPLICANT: Ralos, Michael D. TITLE OF INVENTION: COMPOSITIONS AND FITE DEFENDED AND FITE 
   Fling, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 2239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-738-973-440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2239
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 440
APPLICANT:
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961 GCATAIGCIGGCIGGTITIACCICAACITIGTIACIGAAGAAGIAGAAAAACCCIGAAAAA 1020
                                                                                                                                                                                                                        1021 ACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACA 1080
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               1141 GIGACCITITICIGAGCGGCTACTGGGAAATITCTCATTAGCAGTICCGAICTTGTTGC 1200
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qq	241 A	GCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGAC 30	
ζλ Ph	301 6	GCCTTTTCAGGAAGACGCCTTTTCAGGAAGAGAGAGAGGCACTGAAGAGGAAAGTC 360 	
ko d	61	CTTTACTGAGGGGAGTCTCC	
3 &	21	CCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACG 48	
qa i	21	rccraaggcgrgcrccagaacacggcgcgcgcgcgrgcrrcragaacace 40 mcmaaaacamaamaamaamagaacamagargagagagagagagagagagagagagagagagaga	
oy D	481 (4	
çy da	541	AAGAAATCTGGAGGTCATTACACATATATTTTGGAAGTCTTTGGTCCATTACCAGCTTTT 600 	
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g	601	TACTGCTGTGATATCCCTG 66	
oy Op	661	AATGTGAAATCCCTGAACTTGCG 72º 	
δ ξ	721	CAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATGG 	
6 6 B	781	GCTGGGGCCCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCTGATA 84 CT111111111111111111111111111111111111	
Oy	41	TATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCC 9	
g 2	841	**************************************	
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δλ	961	GCATARGCTGCTGGTTTTACCTCAACTTGTTACTGAAGAAGTAGAAAACCCTGAAAAA 1020 	
Q		ATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCTGAAAAA 102	
oy G	1021	80	
٥y	1081	1016GCCTACTTACGACCATTAATGCTGAGGAGCTGCTGCTGCTTTCAATGCAGTGGCA	
qq	1081	SGCCTACTITACGACCATTAATGCTGAGGAGCTGCTGTTTCAAATGCAGTGGCA 114	
ò	14	GTGACCTTTTCTGAGCGGCTACTGGGAAATTCTCATTAGCAGTTCCGATCTTTGTTGCT 1200	
o a	4 1	GIGACCITIIICIGAAGCGGCIACIACIGGAAAAAAAAAA	
oy D	1201	CYCLCCGCTTGGCTCCATGAACGTGGTGTTTTGCTGTCTCCAGGTTATTCTATGTT 126	
Qy		GCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGAT	
οg	1261	GCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGC	

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2161 AAAAAAAGCATACATCATGATTATGGCAAAGAGGAGAAGGTAGAGCTGTTCTTAAATT 2220
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            1381 CTCGACAGTCTTTGAATTTCCTCAGTTTTGCCAGGTGGCTTTTTATTGGGCTGGCAGTT 1440
                                                          GCTGGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCCTTTCAAGGTGCCA 1500
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; Patent No. US20020110563A1
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APPLICANT: Henderson, Robert A.
APPLICANT: Lodes, Michael J.
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              639749 seqs, 502280978 residues
                                                                                                                  OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence 440, App Sequence 441, App Sequence 441, App Sequence 31, Appl Sequence 31, Appl Sequence 33, Appl Sequence 33, Appl Sequence 52, Appl Sequence 53, Appl Sequence 53, Appl Sequence 63, Appl Sequence 9, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 10, Appl Sequence 11, Appl Sequence 12, Appl Sequence 5, Appl Sequence 6, Appl	ž, 7, 61
SUMMARIES	ID	US-09-854-133-440 US-09-874-133-440 US-09-738-973-441 US-09-738-973-441 US-09-738-973-441 US-10-163-866-31 US-10-163-866-32 US-10-163-866-32 US-10-163-866-32 US-10-163-866-32 US-10-163-866-32 US-10-163-866-32 US-10-163-866-32 US-10-163-866-10	US-10-163-866-7 US-09-919-172-61
	DB	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9
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oю	Query	100.0 902.0 920.0 920.0 984.3 984.3 987.0 98.3 98.3 98.3 98.3 98.3 98.3 98.3 98.3	16.3
	Score	2239 2080:8 2080:8 2080:8 1980:2 11888:0 11454:4 1454:4 1143:4 11373:4 1047:4 379:2 379:2 379:2 366:4	365.4
	Result No.	1 2 2 4 3 3 7 6 8 4 8 8 7 6 8 9 7 6 9 7 6 9 7 6 9 9 9 9 9 9 9 7 6 9 9 9 9	19

e 55 11, 51, 3,	Sequence 1, Appli Sequence 2, Appli Sequence 14, Appl Sequence 15, Appl	20, 16, 13,	Sequence 27, Appl Sequence 26, Appl Sequence 28, Appl Sequence 24, Appl Sequence 22, Appl Sequence 25, Appl	23, 21, 442, 151, 1307 1307
US-10-044-090-555 US-10-163-866-11 US-10-163-866-3 US-10-163-866-3	US-10-163-866-1 US-10-163-866-2 US-10-163-866-14 US-10-163-866-15	10-163-866- 10-163-866- 10-163-866- 09-815-923-	US-10-163-866-26 US-10-163-866-28 US-10-163-866-24 US-10-163-866-22 US-10-163-866-22	US-10-163 866-23 US-10-163 866-21 US-09-864-133-442 US-09-954-531-151 US-09-954-531-151 US-10-163 866-6 US-10-046-935-1307 US-09-878-178-1307
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                                                                  APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Honderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2239; DB 9; Length 2239; 1100.0%; Pred. No. 0; tive 0; Mismatches 0; Indels 0;
                    Sequence 440, Application US/09854133 Publication No. US20020183499A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.09
Matches 2239; Conservative
                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-854-133-440
US-09-854-133-440
                                                                                                                                                                                                                                                                                                      SEQ ID NO 440
LENGTH: 2239
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Db 45080 GGAGGTTGCAGTGACGAGAGGTGCCATTGCACTCCAGCCTGAGTGACAGAGCAAGAC 45139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING FITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS
                                                 GENERAL INFORMATION:
APPLICANT: Chen, H.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: MUTREATING CHROMOSOME-18p RELATED DISORDERS
FILE REPERENCE: 7853-138
CURRENT APPLICATION NUMBER: US/09/268,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.9%; Score 42.8; DB 4; Length 72604; Best Local Similarity 69.4%; Pred. No. 0.34; Matches 75; Conservative 0; Mismatches 27; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:

FILE REPERENCE: 7853-138

CURRENT APPLICATION NUMBER: US/09/657,474

CURRENT FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: 09/268,992

PRIOR FILING DATE: 1999-03-16

PRIOR PLICATION NUMBER: 09/236,134

PRIOR APPLICATION NUMBER: 09/236,134

PRIOR APPLICATION NUMBER: 60/106,056

PRIOR APPLICATION NUMBER: 60/088,312

PRIOR APPLICATION NUMBER: 60/088,312

PRIOR FILING DATE: 1998-06-05

SOFTWARE: FRSELEEQ for Windows Version 3.0

SOFTWARE: FRSELED for Windows Version 3.0
                                                                                                                                                                                                       NAME/KEY: modified_base
LOCATION: all n positions
OTHER INFORMATION: n=a, c, 9, or t
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; Patent No. 6399762
           ; Sequence 7, Application US/09268992
; Patent No. 6342351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chen, H. APPLICANT: Freimer, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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US-09-268-992-7
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APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: ANGREW T: Watt
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OY 5 GTTGAAGTGAGGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAACAGAA 64

Db 54025 GCTGAGATTACACCACTGCACTCCAGCTGACAGTGACAGTCAGACTCCGACTCAAAAATAA 53966
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70.4%; Pred. No. 0.33;
tive 0; Mismatches 22; Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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Best Local Similarity 69.9%; Pred. No. 0.47;
Matches 58; Conservative 0; Mismatches 25; Indels 0
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                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 108127...108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
                                            OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37 FEATURE:
                                                                                                                                        OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                                                                                                                                            LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 TTAAGGAAAAAAGAAAGAAAGAA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .108177
                                                                                                       NAME/KEY: allele
LOCATION: 106918..106966
                                                                                                                                                                                                                                                                                                       .108130
                     NAME/KEY: allele
LOCATION: 106918..106966
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Best Local Similarity
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LENGTH: 70000
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US-09-851-896-3/c
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: polymorphic base insertion of GTTT
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OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
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OTHER INFORMATION: 5-135-155 : polymorphic base insertion
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION: 5-133-375 : polymorphic base insertion
                                                                      OTHER INFORMATION: 5-128-60 : polymorphic base deletion
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LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A
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INFORMATION: 99-1442-224 : Polymorphic base G
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OTHER INFORMATION: 5-145-24 : Polymorphic base A or
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OTHER INFORMATION: 5-130-276 : polymorphic base A
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INFORMATION: 5-135-357 : polymorphic
                                                                                                                                                                                                                                                                                                                                                             : polymorphic
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INFORMATION: 5-136-174
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INFORMATION: 5-140-120
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                                        NAME/KEY: allele
LOCATION: 93714
                                                                                    FEATURE:
NAME/KEY: allele
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NAME/KEY: allele
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LOCATION: 160031
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NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
                                                                              OTHER INFORMATION: Polymorphic fragment 5-124-273 SEQ ID30
                                                                                                                                                                                                NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
                                                                                                                                                              OTHER INFORMATION: Polymorphic fragment 5-124-273 SEQ ID51
                     or
                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
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NAME/KEY: allele
COCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
COCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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LOCATION: 99075.,99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
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NAME/KEY: allele
COCATION: 99094..99140

TREATURE:
COTHER INFORMATION: Polymorphic fragment 5-130-276 SEQ ID56

FEATURE:
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OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
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OTHER INFORMATION: Polymorphic fragment 5-131-395 SEQ ID57
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OTHER INFORMATION: 5-148-352 : polymorphic base
                                 NAME/KEY: allele
                                                                                             NAME/KEY: allele
LOCATION: 103783..103828
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NAME/KEY: allele
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LOCATION: 103783.
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OTHER INFO
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